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Art Unit: 1623 Phone Number: **308-4639** Serial No. **09/483,337**
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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, key words, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and/or abstract..

Title of Invention: See attached copy of claims.

Inventors (please provide full names): See attached copy of claims.

Earliest Priority Filing Date: **01/15/99**

For Sequence Searches only ***Please include all of the pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.***

method for detecting a known genetic polymorphism in DNA or RNA wherein the detection relies on the adjacent, head-to-tail hybridization of a universal oligonucleotide probe and a polymorphic oligonucleotide probe followed by *in situ* chemical ligation of the separate probes to form a single probe,

wherein detection is based on the presence of a **radiolabel present on one or both initially separate probes**; and

wherein the polymorphism probe is optionally **less than 7 nucleotides in length**;

the **first process step being** contacting the target oligonucleotide sequence with the probes which upon hybridization undergo spontaneous chemical ligation as described above; and the second step is detection of the linked probes **Elected claims = 44-48, 50-54 and 56-60.**

SEE SEQUENCE INFORMATION DISCLOSURE if appropriate.

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Bib Data Sheet

SERIAL NUMBER	FILING DATE	CLASS	GROUP ART UNIT	ATTORNEY DOCKET NO.
09/483,337	01/14/2000 RULE	536	1623	220.00040101

APPLICANTS

Eric T. Kool, Stanford, CA ;

** CONTINUING DATA **********

THIS APPLN CLAIMS BENEFIT OF 60/116,059 01/15/1999

** FOREIGN APPLICATIONS **********

IF REQUIRED, FOREIGN FILING LICENSE GRANTED ** 03/28/2000

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		STATE OR COUNTRY	SHEETS DRAWING	TOTAL CLAIMS	INDEPENDENT CLAIMS
Foreign Priority claimed	☐ yes ☐ no	CA	19	62	15
35 USC 119 (a-d) conditions met	☐ yes ☐ no ☐ Met after Allowance				
Verified and Acknowledged	Examiner's Signature Initials				

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TITLE

Compositions and methods for nonenzymatic ligation of oligonucleotides and detection of genetic polymorphisms

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Class	Subclass

WHAT IS CLAIMED IS:

1. A nucleotide comprising a phosphoroselenoate group or a phosphorotelluroate group.

2. An oligonucleotide comprising as its 3' end the nucleotide of claim 1.

3. The oligonucleotide of claim 2 comprising as its 5' end a nucleoside comprising a 5' leaving group.

4. An oligonucleotide comprising a plurality of 2'-deoxyribonucleotides and one ribonucleotide, the ribonucleotide comprising a functional group selected from the group consisting of a phosphorothioate group, a phosphoroselenoate group and a phosphorotelluroate group; wherein the oligonucleotide comprises, as its 3' end, the ribonucleotide.

5. A solid support comprising the oligonucleotide of claim 4.

6. An oligonucleotide comprising at least one 5' bridging phosphoroselenoester or phosphorotelluroester.

7. The oligonucleotide of claim 6 comprising at least one deoxyribonucleotide.

8. The oligonucleotide of claim 6 comprising at least one ribonucleotide.

9. The oligonucleotide of claim 6 wherein at least one 5' bridging phosphoroselenoester or phosphorotelluroester forms a bridge between a deoxyribonucleotide and a ribonucleotide.

10. The oligonucleotide of claim 6 that is circular or linear.

11. A nucleic acid duplex comprising the oligonucleotide of claim 2 hybridized to a complementary oligonucleotide.

12. A nucleoside selected from the group consisting of a 5'-deoxy-5'-iodothymidine (5'-I-T), 5'-deoxy-5'-iodo-2'-deoxycytidine (5'-I-dC), 5'-deoxy-5'-iodo-2'-deoxyadenosine (5'-I-dA), 5'-deoxy-5'-iodo-3-deaza-2'-deoxyadenosine (5'-I-3-deaza-dA), 5'-deoxy-5'-iodo-2'-deoxyguanosine (5'-I-dG), 5'-deoxy-5'-iodo-3-deaza-2'-deoxyguanosine (5'-I-3-deaza-dG), 5'-deoxy-5'-iodouracil (5'-I-U), 5'-deoxy-5'-iodocytidine (5'-I-C), 5'-deoxy-5'-iodoadenosine (5'-I-A), 5'-deoxy-5'-iodo-3-deazaadenosine (5'-I-3-deaza-A), 5'-deoxy-5'-iodoguanosine (5'-I-G) and 5'-deoxy-5'-iodo-3-deazaguanosine (5'-I-3-deaza-G), and the phosphoroamidite derivatives thereof.

13. An oligonucleotide comprising as its 5' end a nucleotide derived form the nucleoside of claim 12.

14. An oligonucleotide comprising a plurality of 2'-deoxyribonucleotides and one ribonucleotide, the ribonucleotide comprising a 5' leaving group; wherein the oligonucleotide comprises, as its 5' end, the ribonucleotide.

15. A solid support comprising the oligonucleotide of claim 14.

16. The solid support of claim 15 further comprising an oligonucleotide comprising a plurality of 2'-deoxyribonucleotides and one ribonucleotide, the ribonucleotide comprising a functional group selected from the group consisting of a phosphorothioate group, a phosphoroselenoate group and a phosphorotelluroate group; wherein the oligonucleotide comprises, as its 3' end, the ribonucleotide

17 ~~16.~~ A solid support comprising at least one oligonucleotide selected from the group consisting of an oligonucleotide comprising a phosphoroselenoate group, an oligonucleotide comprising phosphoroselenoate group, an oligonucleotide comprising a phosphorotelluroate group, and an oligonucleotide comprising a 5' leaving group.

18 ~~17.~~ The solid support of claim 16 comprising an oligonucleotide comprising a 5' leaving group and at least one oligonucleotide selected from the group consisting of an oligonucleotide comprising a phosphoroselenoate group, an oligonucleotide comprising phosphoroselenoate group, an oligonucleotide comprising a phosphorotelluroate group.

19 ~~18.~~ A method for making an oligonucleotide comprising:

binding at least one upstream oligonucleotide and at least one downstream oligonucleotide to a polynucleotide template;

the upstream oligonucleotide comprising, as its 5' end, a nucleoside comprising a 5' leaving group; and

the downstream oligonucleotide comprising, as its 3' end, a nucleoside comprising a 3' phosphoroselenoate or a 3' phosphorotelluroate, wherein the downstream oligonucleotide binds such that it 3' end is substantially adjacent to the 5' end of the upstream oligonucleotide;

to yield an autoligated oligonucleotide product comprising the upstream oligonucleotide ligated to the downstream oligonucleotide.

19. The method of claim 18 where one oligonucleotide comprises a fluorescence energy donor group and the other oligonucleotide comprises a fluorescence energy acceptor group, and wherein the presence or absence of the autoligated oligonucleotide product is accompanied by a detectable change in fluorescence emission of the ligated product compared to the fluorescence energy emissions of the unligated oligonucleotides.

20. A method for detecting a genetic polymorphism in a target polynucleotide comprising:

providing a mutant polymorphism oligonucleotide probe that is complementary to a region on the target polynucleotide that comprises the genetic polymorphism;

providing a universal oligonucleotide probe capable of binding to the target polynucleotide at a region that is conserved in the analogous wild-type polynucleotide;

wherein one oligonucleotide probe constitutes an upstream oligonucleotide comprising, as its 5' end, a nucleoside comprising a 5' leaving group and the other oligonucleotide probe constitutes a downstream oligonucleotide comprising, as its 3' end, a nucleoside comprising a 3' phosphoroselenoate or a 3' phosphorotelluroate, such that, when both probes are bound to the target polynucleotide, an end of the universal oligonucleotide probe is substantially adjacent to an end of the mutant polymorphism oligonucleotide probe so as to position the 5' leaving group and the 3' phosphoroselenoate or a 3' phosphorotelluroate in close proximity to one another;

contacting the target polynucleotide with the universal oligonucleotide probe and the mutant polymorphism oligonucleotide probe to yield an autoligated oligonucleotide product comprising the universal oligonucleotide probe and the mutant polymorphism probe; and

detecting the presence of the autoligated oligonucleotide product.

22 21. The method of claim 20 wherein at least one of the mutant polymorphism oligonucleotide probe and the universal oligonucleotide probe comprises a detectable label.

23 22. The method of claim 21 wherein the detectable label is a radiolabel.

24 23. The method of claim 20 wherein the genetic polymorphism is selected from the group consisting of a single base mutation, a plurality of single base mutations, a deletion, an insertion, and a genetic rearrangement.

25 24. The method of claim 20 wherein the nucleotide position of the genetic polymorphism is not the nucleotide position corresponding to the ligation junction end of the mutant polymorphism probe.

26 25. The method of claim 20 wherein the mutant polymorphism probe is about 3 to about 12 nucleotides in length.

27 26. The method of claim 25 wherein the mutant polymorphism probe is about 3 to about 6 nucleotides in length.

28 21
27. The method of claim 20 wherein the target polynucleotide is DNA or RNA.

29 21
28. The method of claim 20 wherein the target polynucleotide is double-stranded or single-stranded.

30 21
29. The method of claim 20 wherein one oligonucleotide probe comprises a fluorescence energy donor group and the other oligonucleotide comprises a fluorescence energy acceptor group, and wherein the presence or absence of the autoligated oligonucleotide product is accompanied by a detectable change in fluorescence emission of the ligated product compared to the fluorescence emissions of the unligated oligonucleotides.

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30. A method for determining whether a target polynucleotide contains a genetic polymorphism comprising:

providing a mutant polymorphism oligonucleotide probe comprising a first fluorescence energy acceptor group, wherein the mutant polymorphism oligonucleotide probe is complementary to a region on the target polynucleotide that comprises the genetic polymorphism;

providing a wild-type polymorphism oligonucleotide probe comprising a second fluorescence energy acceptor group, wherein the wild-type polymorphism oligonucleotide probe is complementary to a region on the analogous wild-type polynucleotide that is analogous to the region comprising the genetic polymorphism;

providing a universal oligonucleotide probe comprising a fluorescence energy donor group, wherein the universal probe is capable of binding to the target polynucleotide at a region that is conserved in the analogous wild-type polynucleotide;

wherein either (i) the universal oligonucleotide probe constitutes an upstream

oligonucleotide comprising, as its 5' end, a nucleoside comprising a 5' leaving group and both polymorphism oligonucleotide probes constitute downstream oligonucleotides comprising, as their 3' ends, a nucleoside comprising a 3' functional group selected from the group consisting of a 3' phosphorothioate, a 3' phosphoroselenoate and a 3' phosphorotelluroate; or (ii) both polymorphism oligonucleotide probes constitute upstream oligonucleotides comprising, as their 5' ends, a nucleoside comprising a 5' leaving group and the universal oligonucleotide probe constitutes a downstream oligonucleotide comprising, as its 3' end, a nucleoside comprising a 3' functional group selected from the group consisting of a 3' phosphorothioate, a 3' phosphoroselenoate and a 3' phosphorotelluroate;

such that, when a universal probe and a polymorphism probe are bound to the target polynucleotide, an end of the universal oligonucleotide probe is substantially adjacent to an end of the polymorphism oligonucleotide probe so as to position the 5' leaving group and the 3' functional group in close proximity to one another;

contacting the target polynucleotide with the universal oligonucleotide probe, the mutant polymorphism oligonucleotide probe and the wild-type polymorphism oligonucleotide probe to yield an autoligated oligonucleotide product comprising the universal oligonucleotide probe either the mutant polymorphism probe or the wild-type polymorphism oligonucleotide probe;

causing the autoligated oligonucleotide product to fluoresce; and

analyzing the fluorescence emission from the autoligated oligonucleotide product to determine whether the autoligated oligonucleotide product comprises the mutant polymorphism probe or the wild-type polymorphism oligonucleotide probe, wherein the presence of the mutant polymorphism probe in the autoligated oligonucleotide product indicates the presence of a genetic polymorphism in the target polynucleotide.

32 31. The method of claim 31 wherein the genetic polymorphism is selected from the group consisting of a single base mutation, a plurality of single base mutations, a deletion, an insertion, and a genetic rearrangement.

33 32. The method of claim 31 wherein the nucleotide position of the genetic polymorphism is not the nucleotide position corresponding to the ligation junction end of the mutant polymorphism probe.

34 33. The method of claim 31 wherein the mutant polymorphism probe is about 3 to about 12 nucleotides in length.

35 34. The method of claim 33 wherein the mutant polymorphism probe is about 3 to about 6 nucleotides in length.

36 35. The method of claim 31 wherein the target polynucleotide is DNA or RNA.

37 36. The method of claim 31 wherein the target polynucleotide is single-stranded or double-stranded.

38 37. A method for detecting a genetic polymorphism in a target polynucleotide comprising:

providing a mutant polymorphism oligonucleotide probe that is complementary to a region on the target polynucleotide that comprises the genetic polymorphism;

providing a universal oligonucleotide probe capable of binding to the target polynucleotide at a region that is conserved in the analogous wild-type polynucleotide;

wherein one oligonucleotide probe constitutes an upstream oligonucleotide comprising, as its 5' end, a nucleoside comprising a 5' leaving group and the other oligonucleotide probe constitutes a downstream oligonucleotide comprising, as its 3' end, a nucleoside comprising a 3' functional group selected from the group consisting of a 3' phosphorothioate, a 3' phosphoroselenoate and a 3' phosphorotelluroate, such that, when both probes are bound to the target polynucleotide, an end of the universal oligonucleotide probe is substantially adjacent to an end of the mutant polymorphism oligonucleotide probe so as to position the 5' leaving group and the 3' functional group in close proximity to one another;

and wherein one oligonucleotide probe comprises a fluorescence energy donor group and the other oligonucleotide comprises a fluorescence energy acceptor group;

contacting the target polynucleotide with the universal oligonucleotide probe and the mutant polymorphism oligonucleotide probe to yield an autoligated oligonucleotide product comprising the universal oligonucleotide probe and the mutant polymorphism probe; and

detecting the presence or absence of the autoligated oligonucleotide product, wherein the presence or absence of the autoligated oligonucleotide product is accompanied by a detectable change in fluorescence emission of the ligated product compared to the fluorescence emissions of the unligated oligonucleotides.

39 ~~38~~. The method of claim ~~37~~ 38 wherein the nucleotide position of the genetic polymorphism is not the nucleotide position corresponding to the ligation junction end of the mutant polymorphism probe.

40 ~~39~~. The method of claim ~~37~~ 38 wherein the mutant polymorphism probe is about 3 to about 12 nucleotides in length.

111 40. The method of claim 39 wherein the mutant polymorphism probe is about 3 to about 6 nucleotides in length.

112 41. The method of claim 37 wherein the target polynucleotide is DNA or RNA.

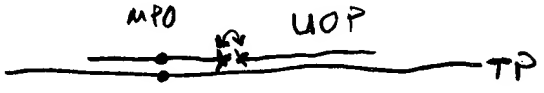
113 42. The method of claim 37 wherein the target polynucleotide is single-stranded or double-stranded.

43. A method for detecting a genetic polymorphism in a target polynucleotide comprising:

providing a mutant polymorphism oligonucleotide probe that is complementary to a region on the target polynucleotide that comprises the genetic polymorphism;

providing a universal oligonucleotide probe capable of binding to the target polynucleotide at a region that is conserved in the analogous wild-type polynucleotide;

wherein one oligonucleotide probe constitutes an upstream oligonucleotide comprising, as its 5' end, a nucleoside comprising a 5' leaving group and the other oligonucleotide probe constitutes a downstream oligonucleotide comprising, as its 3' end, a nucleoside comprising a 3' functional group selected from the group consisting of a 3' phosphorothioate, a 3' phosphoroselenoate and a 3' phosphorotelluroate, such that, when both probes are bound to the target polynucleotide, an end of the universal oligonucleotide probe is substantially but not directly adjacent to an end of the mutant polymorphism oligonucleotide probe so as to position the 5' leaving group and the 3' functional group in close proximity to one another;



contacting the target polynucleotide with the universal oligonucleotide probe and the mutant polymorphism oligonucleotide probe to yield an autoligated oligonucleotide product comprising the universal oligonucleotide probe and the mutant polymorphism probe; and

detecting the presence of the autoligated oligonucleotide product.

44. The method of claim 43 wherein at least one of the mutant polymorphism oligonucleotide probe and the universal oligonucleotide probe comprises a detectable label.

45. The method of claim 44 wherein the detectable label is a radiolabel.

46. The method of claim 43 wherein the genetic polymorphism is selected from the group consisting of a single base mutation, a plurality of single base mutations, a deletion, an insertion, and a genetic rearrangement.

47. The method of claim 43 wherein the nucleotide position of the genetic polymorphism is not the nucleotide position corresponding to the ligation junction end of the mutant polymorphism probe.

48. The method of claim 43 where one oligonucleotide comprises a fluorescence energy donor group and the other oligonucleotide comprises a fluorescence energy acceptor group, and wherein the presence or absence of the autoligated oligonucleotide product is accompanied by a detectable change in fluorescence emission of the ligated product compared to the fluorescence energy emissions of the unligated oligonucleotides.

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49. A method for detecting a genetic polymorphism in a target polynucleotide comprising:

providing a mutant polymorphism oligonucleotide probe of less than 7 nucleotides in length that is complementary to a region on the target polynucleotide that comprises the genetic polymorphism;

providing a universal oligonucleotide probe capable of binding to the target polynucleotide at a region that is conserved in the analogous wild-type polynucleotide;

wherein one oligonucleotide probe constitutes an upstream oligonucleotide comprising, as its 5' end, a nucleoside comprising a 5' leaving group and the other oligonucleotide probe constitutes a downstream oligonucleotide comprising, as its 3' end, a nucleoside comprising a 3' functional group selected from the group consisting of a 3' phosphorothioate, a 3' phosphoroselenoate and a 3' phosphorotelluroate, such that, when both probes are bound to the target polynucleotide, an end of the universal oligonucleotide probe is substantially adjacent to an end of the mutant polymorphism oligonucleotide probe so as to position the 5' leaving group and the 3' functional in close proximity to one another;

contacting the target polynucleotide with the universal oligonucleotide probe and the mutant polymorphism oligonucleotide probe to yield an autoligated oligonucleotide product comprising the universal oligonucleotide probe and the mutant polymorphism probe; and

detecting the presence of the autoligated oligonucleotide product.

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50. The method of claim 49 wherein at least one of the mutant polymorphism oligonucleotide probe and the universal oligonucleotide probe comprises a detectable label.

5251

51. The method of claim 50 wherein the detectable label is a radiolabel.

52. The method of claim 49 wherein the genetic polymorphism is selected from the group consisting of a single base mutation, a plurality of single base mutations, a deletion, an insertion, and a genetic rearrangement.

53. The method of claim 49 wherein the nucleotide position of the genetic polymorphism is not the nucleotide position corresponding to the ligation junction end of the mutant polymorphism probe.

54. The method of claim 49 where one oligonucleotide comprises a fluorescence energy donor group and the other oligonucleotide comprises a fluorescence energy acceptor group, and wherein the presence or absence of the autoligated oligonucleotide product is accompanied by a detectable change in fluorescence emission of the ligated product compared to the fluorescence energy emissions of the unligated oligonucleotides.

55. A method for detecting a genetic polymorphism in a target RNA comprising:

providing a mutant polymorphism oligonucleotide probe that is complementary to a region on the target RNA that comprises the genetic polymorphism;

providing a universal oligonucleotide probe capable of binding to the target RNA at a region that is conserved in the analogous wild-type RNA;

wherein one oligonucleotide probe constitutes an upstream oligonucleotide comprising, as its 5' end, a nucleoside comprising a 5' leaving group and the other oligonucleotide probe constitutes a downstream oligonucleotide comprising, as its 3' end, a nucleoside comprising a 3' functional group selected from the group consisting of a 3' phosphorothioate, a 3' phosphoroselenoate and a 3' phosphorotelluroate, such that, when both probes are bound to the target RNA, an end of the universal oligonucleotide probe is

substantially adjacent to an end of the mutant polymorphism oligonucleotide probe so as to position the 5' leaving group and the 3' functional group in close proximity to one another;

contacting the target RNA with the universal oligonucleotide probe and the mutant polymorphism oligonucleotide probe to yield an autoligated oligonucleotide product comprising the universal oligonucleotide probe and the mutant polymorphism probe; and

detecting the presence of the autoligated oligonucleotide product.

56. The method of claim 55 wherein at least one of the mutant polymorphism oligonucleotide probe and the universal oligonucleotide probe comprises a detectable label.

57. The method of claim 56 wherein the detectable label is a radiolabel.

58. The method of claim 55 wherein the genetic polymorphism is selected from the group consisting of a single base mutation, a plurality of single base mutations, a deletion, an insertion, and a genetic rearrangement.

59. The method of claim 55 wherein the nucleotide position is not the nucleotide position corresponding to the ligation junction end of the mutant polymorphism probe.

60. The method of claim 55 where one oligonucleotide comprises a fluorescence energy donor group and the other oligonucleotide comprises a fluorescence energy acceptor group, and wherein the presence or absence of the autoligated oligonucleotide product is accompanied by a detectable change in fluorescence emission of the ligated product compared to the fluorescence energy emissions of the unligated oligonucleotides.

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61. A method for detecting a genetic polymorphism in a target polynucleotide comprising:

providing a mutant polymorphism oligonucleotide probe that is complementary to a region on the target polynucleotide that comprises the genetic polymorphism;

providing a universal oligonucleotide probe capable of binding to the target polynucleotide at a region that is conserved in the analogous wild-type polynucleotide;

wherein one oligonucleotide probe constitutes an upstream oligonucleotide comprising, as its 5' end, a nucleoside comprising a 5' leaving group and the other oligonucleotide probe constitutes a downstream oligonucleotide comprising, as its 3' end, a nucleoside comprising a 3' phosphoroselenoate or a 3' phosphorotelluroate, such that, when both probes are bound to the target polynucleotide, an end of the universal oligonucleotide probe is substantially adjacent to an end of the mutant polymorphism oligonucleotide probe so as to position the 5' leaving group and the 3' phosphoroselenoate or a 3' phosphorotelluroate in close proximity to one another;

contacting the target polynucleotide with the universal oligonucleotide probe and the mutant polymorphism oligonucleotide probe to yield an autoligated oligonucleotide product comprising the universal oligonucleotide probe and the mutant polymorphism probe; and

detecting the presence of the autoligated oligonucleotide product;

wherein the autoligation is reversible by contacting the autoligated oligonucleotide product with silver or mercuric ions.

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62. A method for detecting a genetic polymorphism in a target polynucleotide comprising:

providing a mutant polymorphism oligonucleotide probe that is complementary to a region on the target polynucleotide that comprises the genetic polymorphism;

providing a universal oligonucleotide probe capable of binding to the target polynucleotide at a region that is conserved in the analogous wild-type polynucleotide;

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wherein one oligonucleotide probe constitutes an upstream oligonucleotide comprising, as its 5' end, a 5'-iodopyrene and the other oligonucleotide probe constitutes a downstream oligonucleotide comprising, as its 3' end, a pyrene nucleoside selected from the group consisting of a 3' phosphorothioate, a 3' phosphoroselenoate and a 3' phosphorotelluroate, such that, when both probes are bound to the target polynucleotide, an end of the universal oligonucleotide probe is substantially adjacent to an end of the mutant polymorphism oligonucleotide probe so as to position the 5'-iodopyrene and the 3' pyrene nucleoside in close proximity to one another;

contacting the target polynucleotide with the universal oligonucleotide probe and the mutant polymorphism oligonucleotide probe to yield an autoligated oligonucleotide product comprising the universal oligonucleotide probe, the mutant polymorphism probe, and a pyrene excimer; and

detecting the presence of the autoligated oligonucleotide product using excimers as labels.

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=> file medline
FILE 'MEDLINE' ENTERED AT 19:55:22 ON 16 JUL 2002

 FILE LAST UPDATED: 16 JUL 2002 (20020716/UP). FILE COVERS 1958 TO DATE.

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 MeSH 2002 vocabulary. Enter HELP THESAURUS for details.

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=> D QUE L3
L1   (     10021) SEA FILE=MEDLINE ABB=ON  PLU=ON . OLIGONUCLEOTIDE PROBES+NT,PFT/
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L2   (       127) SEA FILE=MEDLINE ABB=ON  PLU=ON  ((NON ENZYMAT? OR NONENZYMAT?)
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=> s L3 or L6 or L19 or L22
L176          8 L3 OR L6 OR L19 OR L22

=> file biosis
FILE 'BIOSIS' ENTERED AT 19:56:50 ON 16 JUL 2002
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CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 10 July 2002 (20020710/ED)


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=> D QUE L37
L33 (     47695)SEA FILE=BIOSIS ABB=ON  PLU=ON  OLIGONUCLEOTIDE OR OLIGO
                NUCLEOTIDE OR OLIGORIBONUCLEOTIDE OR OLIGO RIBONUCLEOTIDE OR
                OLIGODEOXYRIBNUCLEOTIDE OR OLIGO DEOXYRIBONUCLEOTIDE OR
                POLYNUCLEOTIDE OR POLY NUCLEOTIDE
L34 (    141766)SEA FILE=BIOSIS ABB=ON  PLU=ON  POLYMORPH?
L35 (        33)SEA FILE=BIOSIS ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3A)
                LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L36 (        18)SEA FILE=BIOSIS ABB=ON  PLU=ON  L33 AND L35
L37           0 SEA FILE=BIOSIS ABB=ON  PLU=ON  L36 AND L34


=> D QUE L41
L38 (     47695)SEA FILE=BIOSIS ABB=ON  PLU=ON  OLIGONUCLEOTIDE OR OLIGO
                NUCLEOTIDE OR OLIGORIBONUCLEOTIDE OR OLIGO RIBONUCLEOTIDE OR
                OLIGODEOXYRIBNUCLEOTIDE OR OLIGO DEOXYRIBONUCLEOTIDE OR
```

```
                POLYNUCLEOTIDE OR POLY NUCLEOTIDE
L39 (        33)SEA FILE=BIOSIS ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3A)
                LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L40 (        18)SEA FILE=BIOSIS ABB=ON  PLU=ON  L38 AND L39
L41           0 SEA FILE=BIOSIS ABB=ON  PLU=ON  L40 AND (LABEL? OR RADIOLABEL?)


=> D QUE L45
L42 (     47695)SEA FILE=BIOSIS ABB=ON  PLU=ON  OLIGONUCLEOTIDE OR OLIGO
                NUCLEOTIDE OR OLIGORIBONUCLEOTIDE OR OLIGO RIBONUCLEOTIDE OR
                OLIGODEOXYRIBNUCLEOTIDE OR OLIGO DEOXYRIBONUCLEOTIDE OR
                POLYNUCLEOTIDE OR POLY NUCLEOTIDE
L43 (        33)SEA FILE=BIOSIS ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3A)
                LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L44 (        18)SEA FILE=BIOSIS ABB=ON  PLU=ON  L42 AND L43
L45           3 SEA FILE=BIOSIS ABB=ON  PLU=ON  L44 AND PROBE


=> D QUE L49
L46 (     47695)SEA FILE=BIOSIS ABB=ON  PLU=ON  OLIGONUCLEOTIDE OR OLIGO
                NUCLEOTIDE OR OLIGORIBONUCLEOTIDE OR OLIGO RIBONUCLEOTIDE OR
                OLIGODEOXYRIBNUCLEOTIDE OR OLIGO DEOXYRIBONUCLEOTIDE OR
                POLYNUCLEOTIDE OR POLY NUCLEOTIDE
L47 (        33)SEA FILE=BIOSIS ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3A)
                LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L48 (        18)SEA FILE=BIOSIS ABB=ON  PLU=ON  L46 AND L47
L49           4 SEA FILE=BIOSIS ABB=ON  PLU=ON  L48 AND TARGET


=> D QUE L55
L50 (     47695)SEA FILE=BIOSIS ABB=ON  PLU=ON  OLIGONUCLEOTIDE OR OLIGO
                NUCLEOTIDE OR OLIGORIBONUCLEOTIDE OR OLIGO RIBONUCLEOTIDE OR
                OLIGODEOXYRIBNUCLEOTIDE OR OLIGO DEOXYRIBONUCLEOTIDE OR
                POLYNUCLEOTIDE OR POLY NUCLEOTIDE
L51 (        33)SEA FILE=BIOSIS ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3A)
                LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L52 (        18)SEA FILE=BIOSIS ABB=ON  PLU=ON  L50 AND L51
L53 (        13)SEA FILE=BIOSIS ABB=ON  PLU=ON  L52 AND (TEMPLATE OR TARGET)
L54 (        10)SEA FILE=BIOSIS ABB=ON  PLU=ON  L53 AND TEMPLATE
L55           7 SEA FILE=BIOSIS ABB=ON  PLU=ON  L54 NOT (CIRCULAR OR HAIPIN OR
                PHOTOLIGATION)


=> D QUE L58
L56 (        33)SEA FILE=BIOSIS ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3A)
                LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L57 (      3800)SEA FILE=BIOSIS ABB=ON  PLU=ON  PHOSPHOROTHIOATE OR PHOSPHORO
                THIOATE OR PHOSPHOROSELENOATE OR PHOSPHORO SELENOATE OR
                PHOSPHOROTELLUROATE OR PHOSPHORO TELLUROATE
L58           6 SEA FILE=BIOSIS ABB=ON  PLU=ON  L57 AND L56


=> s L32 or L45 or L49 or L55 or L58
L177         13 L32 OR L45 OR L49 OR L55 OR L58

=> file biotechno
FILE 'BIOTECHNO' ENTERED AT 19:59:04 ON 16 JUL 2002
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FILE LAST UPDATED: 09 JUL 2002      <20020709/UP>
FILE COVERS 1980 TO DATE.

>>>  SIMULTANEOUS LEFT AND RIGHT TRUNCATION AVAILABLE IN
     /CT AND BASIC INDEX  <<<

=> D QUE L65
L59 (     30360)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  OLIGONUCLEOTIDE OR OLIGO
                NUCLEOTIDE OR OLIGORIBONUCLEOTIDE OR OLIGO RIBONUCLEOTIDE OR
                OLIGODEOXYRIBNUCLEOTIDE OR OLIGO DEOXYRIBONUCLEOTIDE OR
                POLYNUCLEOTIDE OR POLY NUCLEOTIDE
L60 (    100433)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  HYBRIDIZ? OR HYBRIDIS?
L61 (     60424)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  POLYMORPH?
L62 (      8328)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  L59 AND L60
L63 (       811)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  L61 AND L62
L64 (        24)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3
                A) LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L65           0 SEA FILE=BIOTECHNO ABB=ON  PLU=ON  L63 AND L64


=> D QUE L68
L66 (     60424)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  POLYMORPH?
L67 (        24)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3
                A) LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L68           0 SEA FILE=BIOTECHNO ABB=ON  PLU=ON  L66 AND L67


=> D QUE L71
L69 (    100433)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  HYBRIDIZ? OR HYBRIDIS?
L70 (        24)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3
                A) LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L71           4 SEA FILE=BIOTECHNO ABB=ON  PLU=ON  L69 AND L70


=> D QUE L75
L72 (     30360)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  OLIGONUCLEOTIDE OR OLIGO
                NUCLEOTIDE OR OLIGORIBONUCLEOTIDE OR OLIGO RIBONUCLEOTIDE OR
                OLIGODEOXYRIBNUCLEOTIDE OR OLIGO DEOXYRIBONUCLEOTIDE OR
                POLYNUCLEOTIDE OR POLY NUCLEOTIDE
L73 (        24)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3
                A) LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L74 (        12)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  L72 AND L73
L75           7 SEA FILE=BIOTECHNO ABB=ON  PLU=ON  L74 NOT (CIRCULAR OR HAIPIN
                OR PHOTOLIGATION)


=> D QUE L78
L76 (        24)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3
                A) LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L77 (      2060)SEA FILE=BIOTECHNO ABB=ON  PLU=ON  PHOSPHOROTHIOATE OR
                PHOSPHORO THIOATE OR PHOSPHOROSELENOATE OR PHOSPHORO SELENOATE
                OR PHOSPHOROTELLUROATE OR PHOSPHORO TELLUROATE
L78           3 SEA FILE=BIOTECHNO ABB=ON  PLU=ON  L76 AND L77


=> s L71 or L75 or L78
L178         10 L71 OR L75 OR L78

=> file hcaplus
FILE 'HCAPLUS' ENTERED AT 20:00:44 ON 16 JUL 2002
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FILE COVERS 1907 - 16 Jul 2002 VOL 137 ISS 3
FILE LAST UPDATED: 15 Jul 2002 (20020715/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

```
=> D QUE L90
L79 (     12146)SEA FILE=HCAPLUS ABB=ON  PLU=ON  "PROBES (NUCLEIC ACID)"+NT,PFT
                /CT
L80 (      7118)SEA FILE=HCAPLUS ABB=ON  PLU=ON  OLIGODEOXYRIBONUCLEOTIDES+NT,P
                FT/CT
L81 (     21465)SEA FILE=HCAPLUS ABB=ON  PLU=ON  NUCLEIC ACID HYBRIDIZATION+NT,
                PFT/CT
L82 (    205562)SEA FILE=HCAPLUS ABB=ON  PLU=ON  RNA+NT,PFT/CT
L83 (    250014)SEA FILE=HCAPLUS ABB=ON  PLU=ON  DNA+NT,PFT/CT
L84 (     30363)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (L82 OR L83) (L) (ANT OR
                ANST)/RL
L85 (      5357)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L84 AND L81
L86 (       663)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (L79 OR L80) (L) (RACT OR
                RCT)/RL
L87 (     10873)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (L79 OR L80) (L) (ANST OR
                ARG)/RL
L88 (        46)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L86 AND L87
L89 (        10)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L88 AND L85
L90           1 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L89 AND (?LIGAT? OR LIGAT?)
```

ANT = Analyte role
ANST = Analytical study
RACT = Reactant or Reagent
RCT = Reactant

```
=> D QUE L100
L91 (     12146)SEA FILE=HCAPLUS ABB=ON  PLU=ON  "PROBES (NUCLEIC ACID)"+NT,PFT
                /CT
L92 (      7118)SEA FILE=HCAPLUS ABB=ON  PLU=ON  OLIGODEOXYRIBONUCLEOTIDES+NT,P
                FT/CT
L93 (     21465)SEA FILE=HCAPLUS ABB=ON  PLU=ON  NUCLEIC ACID HYBRIDIZATION+NT,
                PFT/CT
L94 (    205562)SEA FILE=HCAPLUS ABB=ON  PLU=ON  RNA+NT,PFT/CT
L95 (    250014)SEA FILE=HCAPLUS ABB=ON  PLU=ON  DNA+NT,PFT/CT
L96 (     30363)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (L94 OR L95) (L) (ANT OR
                ANST)/RL
L97 (      5357)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L96 AND L93
L98 (      9577)SEA FILE=HCAPLUS ABB=ON  PLU=ON  AUTOLIGATION OR AUTO LIGATION
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```
                OR SELF LIGATION OR AUTOCATALY? OR AUTO CATALY?
L99 (         20)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L98 AND (L91 OR L92)
L100           2 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L99 AND L97


=> D QUE L103
L101(       9577)SEA FILE=HCAPLUS ABB=ON  PLU=ON  AUTOLIGATION OR AUTO LIGATION
                OR SELF LIGATION OR AUTOCATALY? OR AUTO CATALY?
L102(      47687)SEA FILE=HCAPLUS ABB=ON  PLU=ON  GENETIC POLYMORPHISM+NT,PFT/CT

L103           2 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L101 AND L102


=> D QUE L106
L104(      16231)SEA FILE=HCAPLUS ABB=ON  PLU=ON  COUPLING REACTION+NT,PFT/CT
L105(         43)SEA FILE=HCAPLUS ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3A)
                LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L106           3 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L105 AND L104


=> D QUE L109
L107(      12146)SEA FILE=HCAPLUS ABB=ON  PLU=ON  "PROBES (NUCLEIC ACID)"+NT,PFT
                /CT
L108(         43)SEA FILE=HCAPLUS ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3A)
                LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L109           4 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L107 AND L108


=> D QUE L112
L110(       7118)SEA FILE=HCAPLUS ABB=ON  PLU=ON  OLIGODEOXYRIBONUCLEOTIDES+NT,P
                FT/CT
L111(         43)SEA FILE=HCAPLUS ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3A)
                LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L112          12 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L110 AND L111


=> D QUE L115
L113(         43)SEA FILE=HCAPLUS ABB=ON  PLU=ON  ((NON ENZYM? OR NONENZYM?)(3A)
                LIGAT?) OR (AUTOLIGAT? OR AUTO LIGAT?)
L114(       7797)SEA FILE=HCAPLUS ABB=ON  PLU=ON  PHOSPHOROTHIOATE OR PHOSPHORO
                THIOATE OR PHOSPHOROSELENOATE OR PHOSPHORO SELENOATE OR
                PHOSPHOROTELLUROATE OR PHOSPHORO TELLUROATE
L115           8 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L114 AND L113


=> s L90 or L100 or L103 or L106 or L109 or L112 or L115
L179          21 L90 OR L100 OR L103 OR L106 OR L109 OR L112 OR L115

=> file wpids
FILE 'WPIDS' ENTERED AT 20:02:48 ON 16 JUL 2002
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FILE LAST UPDATED: 11 JUL 2002              <20020711/UP>
MOST RECENT DERWENT UPDATE            200244   <200244/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

>>> The BATCH option for structure searches has been
    enabled in WPINDEX/WPIDS and WPIX  >>>

>>> PATENT IMAGES AVAILABLE FOR PRINT AND DISPLAY >>>
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>>> FOR DETAILS OF THE PATENTS COVERED IN CURRENT UPDATES,
    SEE http://www.derwent.com/dwpi/updates/dwpicov/index.html <<<

>>> FOR A COPY OF THE DERWENT WORLD PATENTS INDEX STN USER GUIDE,
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 http://www.stn-international.de/training_center/patents/stn_guide.pdf <<<

>>> FOR INFORMATION ON ALL DERWENT WORLD PATENTS INDEX USER
    GUIDES, PLEASE VISIT:
    http://www.derwent.com/userguides/dwpi_guide.html <<<

=> D QUE L126
L116(      3744)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGAT?
L117(     78501)SEA FILE=WPIDS ABB=ON  PLU=ON  PROBE OR OLIGONUCLEOTIDE OR
                 OLIGO NUCELOTIDE OR OLIGODEOXYRIBONUCLEOTIDE OR OLIGO DEOXYRIBO
                 NUCLEOTIDE OR OLIGORIBONUCLEOTIDE OR OLIGO RIBONUCLEOTIDE
L118(       716)SEA FILE=WPIDS ABB=ON  PLU=ON  L116 AND L117
L119(     18363)SEA FILE=WPIDS ABB=ON  PLU=ON  HYBRIDIZ? OR HYBRIDIS?
L120(       456)SEA FILE=WPIDS ABB=ON  PLU=ON  L118 AND L119
L121(     19179)SEA FILE=WPIDS ABB=ON  PLU=ON  POLYMORPH? OR POLY MORPH? OR
                 MUTANT OR MUTAT?
L122(       197)SEA FILE=WPIDS ABB=ON  PLU=ON  L120 AND L121
L123(    644604)SEA FILE=WPIDS ABB=ON  PLU=ON  AUTOLIGAT? OR AUTO LIGAT? OR
                 COUPL? OR NONENZYM? OR NON ENZYM?
L124(        20)SEA FILE=WPIDS ABB=ON  PLU=ON  L122 AND L123
L125(      1194)SEA FILE=WPIDS ABB=ON  PLU=ON  PHOSPHOROTHIOATE OR PHOSPHOROSEL
                 ENOATE OR PHOSPHOROTELLUROATE OR PHOSPHORO (W) (THIOATE OR
                 SELENOATE OR TELLUROATE)
L126          1 SEA FILE=WPIDS ABB=ON  PLU=ON  L124 AND L125


=> D QUE L137
L127(      3744)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGAT?
L128(     78501)SEA FILE=WPIDS ABB=ON  PLU=ON  PROBE OR OLIGONUCLEOTIDE OR
                 OLIGO NUCELOTIDE OR OLIGODEOXYRIBONUCLEOTIDE OR OLIGO DEOXYRIBO
                 NUCLEOTIDE OR OLIGORIBONUCLEOTIDE OR OLIGO RIBONUCLEOTIDE
L129(       716)SEA FILE=WPIDS ABB=ON  PLU=ON  L127 AND L128
L130(     18363)SEA FILE=WPIDS ABB=ON  PLU=ON  HYBRIDIZ? OR HYBRIDIS?
L131(       456)SEA FILE=WPIDS ABB=ON  PLU=ON  L129 AND L130
L132(     19179)SEA FILE=WPIDS ABB=ON  PLU=ON  POLYMORPH? OR POLY MORPH? OR
                 MUTANT OR MUTAT?
L133(       197)SEA FILE=WPIDS ABB=ON  PLU=ON  L131 AND L132
L134(    644604)SEA FILE=WPIDS ABB=ON  PLU=ON  AUTOLIGAT? OR AUTO LIGAT? OR
                 COUPL? OR NONENZYM? OR NON ENZYM?
L135(        20)SEA FILE=WPIDS ABB=ON  PLU=ON  L133 AND L134
L136(      3976)SEA FILE=WPIDS ABB=ON  PLU=ON  LEAVING GROUP
L137          1 SEA FILE=WPIDS ABB=ON  PLU=ON  L135 AND L136


=> D QUE L146
L138(     78501)SEA FILE=WPIDS ABB=ON  PLU=ON  PROBE OR OLIGONUCLEOTIDE OR
                 OLIGO NUCELOTIDE OR OLIGODEOXYRIBONUCLEOTIDE OR OLIGO DEOXYRIBO
                 NUCLEOTIDE OR OLIGORIBONUCLEOTIDE OR OLIGO RIBONUCLEOTIDE
L139(    644604)SEA FILE=WPIDS ABB=ON  PLU=ON  AUTOLIGAT? OR AUTO LIGAT? OR
                 COUPL? OR NONENZYM? OR NON ENZYM?
L140(      1194)SEA FILE=WPIDS ABB=ON  PLU=ON  PHOSPHOROTHIOATE OR PHOSPHOROSEL
                 ENOATE OR PHOSPHOROTELLUROATE OR PHOSPHORO (W) (THIOATE OR
                 SELENOATE OR TELLUROATE)
L141(      3976)SEA FILE=WPIDS ABB=ON  PLU=ON  LEAVING GROUP
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L142(     12516)SEA FILE=WPIDS ABB=ON  PLU=ON  POLYNUCLEOTIDE OR POLY NUCLEOTID
                E
L143(     85164)SEA FILE=WPIDS ABB=ON  PLU=ON  L138 OR L142
L144(      7786)SEA FILE=WPIDS ABB=ON  PLU=ON  L139 AND L143
L145(         5)SEA FILE=WPIDS ABB=ON  PLU=ON  L144 AND L141 AND L140
L146          0 SEA FILE=WPIDS ABB=ON  PLU=ON  L145 AND LABEL?


=> D QUE L147
L147          2 SEA FILE=WPIDS ABB=ON  PLU=ON  LIGATION DETECTION REACTION


=> D QUE L148
L148          2 SEA FILE=WPIDS ABB=ON  PLU=ON  LIGATION DEPENDENT AMPLIFICATION


=> D QUE L149
L149          1 SEA FILE=WPIDS ABB=ON  PLU=ON  LIGATION MEDIATED AMPLIFICATION


=> D QUE L162
L150(     19179)SEA FILE=WPIDS ABB=ON  PLU=ON  POLYMORPH? OR POLY MORPH? OR
                MUTANT OR MUTAT?
L151(      3976)SEA FILE=WPIDS ABB=ON  PLU=ON  LEAVING GROUP
L152(         2)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGATION DETECTION REACTION
L153(         2)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGATION DEPENDENT AMPLIFICATION

L154(         1)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGATION MEDIATED AMPLIFICATION

L155(        42)SEA FILE=WPIDS ABB=ON  PLU=ON  OLIGONUCLEOTIDE LIGATION ASSAY
L156(       160)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGASE CHAIN REACTION
L157(         1)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGATION AMPLIFICATION REACTION

L158(       202)SEA FILE=WPIDS ABB=ON  PLU=ON  (L152 OR L153 OR L154 OR L155
                OR L156 OR L157)
L159(    588608)SEA FILE=WPIDS ABB=ON  PLU=ON  INSERT? OR DELET? OR REARRANG?
L160(    604201)SEA FILE=WPIDS ABB=ON  PLU=ON  L159 OR L150
L161(        91)SEA FILE=WPIDS ABB=ON  PLU=ON  L158 AND L160
L162          0 SEA FILE=WPIDS ABB=ON  PLU=ON  L161 AND L151


=> D QUE L175
L163(     19179)SEA FILE=WPIDS ABB=ON  PLU=ON  POLYMORPH? OR POLY MORPH? OR
                MUTANT OR MUTAT?
L164(      1194)SEA FILE=WPIDS ABB=ON  PLU=ON  PHOSPHOROTHIOATE OR PHOSPHOROSEL
                ENOATE OR PHOSPHOROTELLUROATE OR PHOSPHORO (W) (THIOATE OR
                SELENOATE OR TELLUROATE)
L165(         2)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGATION DETECTION REACTION
L166(         2)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGATION DEPENDENT AMPLIFICATION

L167(         1)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGATION MEDIATED AMPLIFICATION

L168(        42)SEA FILE=WPIDS ABB=ON  PLU=ON  OLIGONUCLEOTIDE LIGATION ASSAY
L169(       160)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGASE CHAIN REACTION
L170(         1)SEA FILE=WPIDS ABB=ON  PLU=ON  LIGATION AMPLIFICATION REACTION

L171(       202)SEA FILE=WPIDS ABB=ON  PLU=ON  (L165 OR L166 OR L167 OR L168
                OR L169 OR L170)
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similar methods but require ligase.

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L172(    588608)SEA FILE=WPIDS ABB=ON  PLU=ON  INSERT? OR DELET? OR REARRANG?
L173(    604201)SEA FILE=WPIDS ABB=ON  PLU=ON  L172 OR L163
L174(        91)SEA FILE=WPIDS ABB=ON  PLU=ON  L171 AND L173
L175          0 SEA FILE=WPIDS ABB=ON  PLU=ON  L174 AND L164


=> s L126 or L137 or L147 or L148 or L149
L180          6 L126 OR L137 OR L147 OR L148 OR L149

=> dup rem L176-180
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FILE 'BIOSIS' ENTERED AT 20:05:20 ON 16 JUL 2002
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PROCESSING COMPLETED FOR L176
PROCESSING COMPLETED FOR L177
PROCESSING COMPLETED FOR L178
PROCESSING COMPLETED FOR L179
PROCESSING COMPLETED FOR L180
L181         33 DUP REM L176-180 (25 DUPLICATES REMOVED)

=> d ibib ab 1-33
```

L181 ANSWER 1 OF 33 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:522052 HCAPLUS
TITLE: 5'-thio phosphate directed ligation of oligonucleotides and use in detection of single nucleotide polymorphisms
INVENTOR(S): Bandaru, Rajanikanth; Kumar, Gyanendra
PATENT ASSIGNEE(S): Molecular Staging, Inc., USA
SOURCE: PCT Int. Appl.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002053780	A2	20020711	WO 2002-US200005	20020104

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2001-259918P P 20010105
US 2001-910372 A 20010720

AB The present invention provides a novel method for ligation of oligonucleotides containing 5'-**phosphorothioates** on complementary templates by the action of DNA ligases. This reaction is readily applied to the synthesis of a single stranded circular DNA containing a **phosphorothioate** directed ligation reaction by ATP dependent DNA ligase reaction is similar to conventional 5'-phosphate ligation. The utility of enzymatic ligation in probing specific sequences of DNA is also described. The present invention also provides a novel **non-enzymatic ligation** of 5'-**phosphorothioates** that has been applied to the synthesis of single strand **phosphorothioate** and phosphate circular DNA. A process for detecting the presence of a mismatch in an otherwise complementary pair of oligonucleotides is disclosed using an enzyme-based technique which shows the presence of a mismatch by failing to form a ligated single stranded DNA circle that can optionally be amplified using standard methods of rolling circle amplification.

L181 ANSWER 2 OF 33 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:172144 HCAPLUS
DOCUMENT NUMBER: 136:227889
TITLE: Gene analysis via thermocycling hybridization-ligation-denaturation reaction using double-stranded polymer-forming Honeycomb probes that cross in alternation.
INVENTOR(S): Usui, Mitsugu; Mitsuka, Mari; Hakii, Chikako
PATENT ASSIGNEE(S): Sanko Junyaku Co., Ltd., Japan
SOURCE: PCT Int. Appl., 65 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002018642	A1	20020307	WO 2001-JP7020	20010814

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: JP 2000-261687 A 20000830

AB A method for target gene detection using polymers of hybridization probes without using any enzyme and the need for capturing ligated oligonucleotides or washing excess oligonucleotides, is disclosed. A double-stranded probe polymer is formed by hybridizing plural probe pairs, each consisting of a pair of probes having n (n .gtoreq. 3) base sequence regions complementary to each other, described as Honeycomb probes (HCP) in such a manner as to form alternate crossing. One or more points in one or both sides of the complementary region of a target gene of the above-described probe pair, are preliminarily cleaved and then a hybridization reaction, a ligation reaction and a dissocn. reaction are conducted under temp. regulation using a thermocycler. The cleaved probes are ligated to form a complete probe using DNA ligase or **autoligation**. A complex of a target gene with the probe polymer is formed by using a base sequence complementary to a part of the target gene as one of the complementary regions of the probe and thus the target gene is assayed. The process is termed PALSAR (Probe alternation link self-assembly reaction) and can be used to detect single nucleotide polymorphisms (SNPs). Single or double-stranded DNA, or RNA, can be used as target. Preferably, the probes are labeled with a quencher and a fluorophore at one of both ends.

REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L181 ANSWER 3 OF 33 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:158019 HCAPLUS
DOCUMENT NUMBER: 136:180144
TITLE: Methods and compositions for ultra low copy number analyte detection by zymogen mediated signal amplification
INVENTOR(S): Ramberg, Elliot R.
PATENT ASSIGNEE(S): Cygene, Inc., USA
SOURCE: PCT Int. Appl., 54 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002016634	A1	20020228	WO 2001-US26231	20010822

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,

US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.: US 2000-226823P P 20000822
AB The present invention is directed to methods and compns. for signal amplification used in analyzing large quantities of a DNA, protein, cellular or RNA sample to detect a target analyte. The methods of the present invention, Zymogen Mediated Signal Amplification, ZMSA, minimize the occurrence of false pos. and false neg. conclusions in diagnostic results without DNA amplification or reverse transcriptase reactions. The signal amplification methods of the present invention employ highly increased signal prodn. capabilities of an enzyme and its substrate. Embodiments of the present invention may take the form of an **autocatalytic** reaction or a synthetic enzyme. Figure (1) is a chart showing signal generation by Zymogen Mediated Signal Amplification (ZMSA-1).
REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L181 ANSWER 4 OF 33 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002146636 MEDLINE
DOCUMENT NUMBER: 21871128 PubMed ID: 11878946
TITLE: Quencher as leaving group: efficient detection of DNA-joining reactions.
AUTHOR: Sando Shinsuke; Kool Eric T
CORPORATE SOURCE: Department of Chemistry, Stanford University, Stanford, California 94305-5080, USA.
CONTRACT NUMBER: GM62658 (NIGMS)
SOURCE: JOURNAL OF THE AMERICAN CHEMICAL SOCIETY, (2002 Mar 13) 124 (10) 2096-7.
Journal code: 7503056. ISSN: 0002-7863.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200207
ENTRY DATE: Entered STN: 20020307
Last Updated on STN: 20020702
Entered Medline: 20020701
AB We describe a new fluorescence reporting strategy in which dabsyl, a well-known quencher, activates a hydroxyl group in a probe to convert it to a leaving group. When a nucleophilic **phosphorothioate** probe binds adjacent to a dabsyl quenched probe, **autoligation** occurs, releasing the quencher, and lighting up the probes, This signal change can be used to detect single nucleotide differences in DNA without enzymes or reagents.

L181 ANSWER 5 OF 33 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2002-114362 [15] WPIDS
DOC. NO. CPI: C2002-035111
TITLE: Detecting target nucleic acids for identifying splice variants in a target nucleic acid sequence, comprises utilizing **coupled-ligation** and amplification.
DERWENT CLASS: B04 D16
INVENTOR(S): SCHROTH, G P; WENZ, H
PATENT ASSIGNEE(S): (PEKE) PE CORP NY
COUNTRY COUNT: 96
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001092579	A2	20011206	(200215)*	EN	99
AU 2001065121	A	20011211	(200225)		

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001092579	A2	WO 2001-US17329	20010530
AU 2001065121	A	AU 2001-65121	20010530

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001065121	A	Based on	WO 200192579

PRIORITY APPLN. INFO: US 2000-724755 20001128; US 2000-584905 20000530

AB WO 200192579 A UPAB: 20020306

NOVELTY - Detecting (M1) target sequence(s) in a sample by utilizing a **coupled ligation** and amplification reaction, is new.

DETAILED DESCRIPTION - Detecting (M1) target sequence(s) in a sample comprises:

(a) combining the sample with a **probe** set for each target sequence (TS), the **probe** set comprising a **probe** (P1) comprising a target-specific portion (TSP) and a 5' primer-specific portion or TSP alone, and another **probe** (P2) comprising a TSP and a 3' primer-specific portion, where the **probes** in each set are suitable for **ligation** together when **hybridized** adjacent to one another on a complementary TS, and at least one **probe** in each **probe** set further comprises an addressable support-specific portion located between the primer-specific portion and the TSP to form a **ligation** reaction mixture (RM1);

(b) subjecting RM1 to a cycle of **ligation**, where adjacently **hybridizing** complementary **probes** are **ligated** to one another to form a **ligation** product comprising the 5' primer-specific portion, the TSPs, an addressable support-specific portion(s), and the 3' primer-specific portion or a product comprising the above mixture without the 5' primer-specific portion;

(c) combining the RM1 with a primer set comprising a primer (PR1) having a sequence of the 5' primer-specific portion of the **ligation** product, and another primer (PR2) having a sequence complementary to the 3' primer-specific portion of the **ligation** product, where one of the primers comprises a reporter group (RPG), or with a primer comprising a sequence complementary to the primer-specific portion of the **ligation** product and a RPG, and a polymerase to form a first amplification reaction mixture (RM2);

(d) subjecting RM2 to a cycle of amplification to generate a first amplification product (F AmpP) comprising a RPG;

(e) **hybridizing** the addressable support-specific portions of the F AmpP or a portion of the product comprising a RPG to

support-bound capture **oligonucleotides**; and
(f) detecting the RPG.
Optionally M1 is performed by:
(i) combining RM1 to the primer set containing primers which do not contain RPG, then subjecting RM1 to a cycle of amplification to generate F AmpP, followed by combining the obtained product with a primer or primer set comprising RPG to form a second amplification mixture (RM3), which is then subjected to another cycle of amplification and finally step (e) was carried out with the product (S AmpP) obtained, or RPG is detected directly in S AmpP comprising RPG without performing step (e); and
(ii) RPG is detected directly in F AmpP comprising RPG obtained in step (d) after a separation process without performing step (e).
INDEPENDENT CLAIMS are also included for the following:
(1) a **probe** (P) suitable for **ligation** comprising a 5'-end, a 3'-end, a TSP, a primer-specific portion, and an addressable support-specific portion located between the primer-specific portion and TSP; and
(2) a kit (I) for M1 comprising at least one **probe** set for each TS to be detected, the **probe** set comprising P1 having a TSP and a 5' primer-specific portion, and P2 having a TSP and a 3' primer-specific portion, and optionally, a **ligation** agent.
USE - (M1) is useful for detecting target sequence(s) in a sample. The method is useful for identifying splice variants in a target sequence (TS), where the TS comprises complementary DNA (cDNA) generated from an RNA, preferably mRNA, or an RNA target present in the sample, and the **ligation** reaction composition further comprises T4 DNA ligase, the polymerase is DNA dependent DNA polymerase, analyzing comprises **hybridizing** an addressable support-specific portion of a reaction mixture (RM2) or a portion of it comprising a reporter group (RPG) directly or indirectly and further comprises denaturing F AmpP to generate single stranded portions of amplification products (claimed).
ADVANTAGE - Unlike prior art methods, M1 is rapid, reliable and economical.
Dwg.0/6

L181 ANSWER 6 OF 33 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2001-550053 [61] WPIDS
DOC. NO. CPI: C2001-163716
TITLE: An improved multiplex **ligation-dependent amplification** method for detecting specific single stranded target nucleic acids in samples.
DERWENT CLASS: B04 D16
INVENTOR(S): SCHOUTEN, J P
PATENT ASSIGNEE(S): (SCHO-I) SCHOUTEN J P
COUNTRY COUNT: 95
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001061033	A2	20010823	(200161)*	EN	157
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
EP 1130113	A1	20010905	(200161)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					

AU 2001046439 A 20010827 (200176)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001061033	A2	WO 2001-EP1739	20010215
EP 1130113	A1	EP 2000-200506	20000215
AU 2001046439	A	AU 2001-46439	20010215

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001046439	A	Based on	WO 200161033

PRIORITY APPLN. INFO: EP 2000-200506 20000215

AB WO 200161033 A UPAB: 20011024

NOVELTY - An improved multiplex **ligation-dependent amplification** method for detecting specific single stranded target nucleic acids in samples using a number of probe sets comprising at least 2 probes (each comprising a target specific region and a non-complementary region comprising a primer binding site). The probes in each set are ligated when hybridized to a target nucleic acid and amplified by a primer set.

DETAILED DESCRIPTION - A method (I) for detecting in a sample (comprising a number of sample nucleic acids (SNAs) with different sequences), the presence of at least 1 specific single stranded target nucleic acid sequence comprising 2 segments ((S1) and (S2), and optionally a third segment (S3) between S1 and S2 and the segments are adjacent to each other), comprising in a reaction mixture:

(1) contacting the SNAs with a number of different probe sets, each of which comprises:

(a) a first nucleic acid probe (NAP1), comprising:

(i) a first target specific region (TSR1) complementary to S1 of the target nucleic acid sequence (TNAS); and

(ii) a first non-complementary region, 3' from the first region, which is non-complementary to the TNAS, comprising a first tag sequence (TS1);

(b) a second nucleic acid probe (NAP2), comprising:

(i) a second target specific region (TSR2) complementary to S2 of the TNAS; and

(ii) a second non-complementary region, 5' from the second region, which is non-complementary to the TNAS, comprising a second tag sequence (TS2); and

(c) (optionally) a third nucleic acid probe (NAP3) comprising a third target specific region (TSR3) complementary to S3;

(2) incubating the SNAs with the probes allowing hybridization of complementary nucleic acids;

(3) connecting to one another NAP1, NAP2 (and optionally NAP3) hybridized to S1, S2 (and optionally S3) of the same TNAS (respectively) (the hybridized probes are located adjacent to one another, forming an interconnected probe assembly);

(4) amplifying the connected probe assemblies (amplification is initiated by binding of a first nucleic acid primer specific for TS1 followed by elongation); and

(5) detecting an amplicon (the amount of NAP1 is less than 40 femtomoles and the molar ratio between the first nucleic acid primer and NAP1 is at least 200).

INDEPENDENT CLAIMS are also included for the following:

(A) a nucleic acid probe set (II) for use in (I) (the probes are capable of hybridizing to adjacent sites on a DNA sequence which is complementary to a naturally occurring mRNA but have separate target sequences on chromosomal DNA);
(B) a nucleic acid probe (III) for use in (I);
(C) a mixture (IV) of nucleic acids comprising at least 2 (III)s;
(D) a kit (V) for performing (I) comprising (III) and/or (IV); and
(E) a method (VI) for ligating at least 2 nucleic acids to each other, comprising incubating a sample comprising the nucleic acids with a thermostable nucleic acid ligation enzyme under suitable conditions (the ligation enzyme is inactivated by incubating the sample for 10 minutes at approx. 95 deg. C).
USE - The method (I) is used for:
(1) detecting a nucleotide polymorphism, especially a single nucleotide polymorphism;
(2) detecting multiple single stranded TNASs (through the detection of multiple amplicons);
(3) determining the absolute or relative abundance of multiple single stranded nucleic acids in a sample; and
(4) detection of a break point region in rearranged nucleic acids (claimed).
ADVANTAGE - By using a femtomolar amount of the probes a large number of different probe sets can be used to simultaneously detect and quantify a corresponding large number of target sequences with high specifically.
Dwg.0/28

L181 ANSWER 7 OF 33 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2001-138150 [14] WPIDS
DOC. NO. CPI: C2001-040692
TITLE: Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette **ligation-mediated amplification** of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding activity.
DERWENT CLASS: B04 D16
INVENTOR(S): IZUI, M; KURAHASHI, O; NAKAMATSU, T; SUGIMOTO, M
PATENT ASSIGNEE(S): (AJIN) AJINOMOTO CO INC
COUNTRY COUNT: 95
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001002584	A1	20010111	(200114)*	JA	45

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2000055713 A 20010122 (200125)
EP 1197555 A1 20020417 (200233) EN
R: AL BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001002584	A1	WO 2000-JP4348	20000630
AU 2000055713	A	AU 2000-55713	20000630

EP 1197555 A1 EP 2000-940903 20000630
WO 2000-JP4348 20000630

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000055713	A	Based on	WO 200102584
EP 1197555	A1	Based on	WO 200102584

PRIORITY APPLN. INFO: JP 1999-189512 19990702
AB WO 200102584 A UPAB: 20010312
NOVELTY - Proteins comprising either (A) a 661 amino acid sequence (S1) given in the specification or (B) a protein with the amino-acid sequence (S1) but with some amino-acids substituted, deleted, inserted, added or inverted and having sucrose-binding activity, is new. The coryneform bacteria produced using it can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity.
DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a DNA encoding the proteins (A) or (B).
USE - The obtained sucrose PTS (phosphoenolpyruvate-sugar transport system) gene and it's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved amino-acid and nucleic acid productivity.
ADVANTAGE - The produced coryneform bacteria can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity.
Dwg.0/2

L181 ANSWER 8 OF 33 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2001528629 MEDLINE
DOCUMENT NUMBER: 21459024 PubMed ID: 11574689
TITLE: New chemically reactive dsDNAs containing single internucleotide monophosphoryldithio links: reactivity of 5'-mercapto-oligodeoxyribonucleotides.
AUTHOR: Metelev V G; Borisova O A; Volkov E M; Oretskaya T S; Dolinnaya N G
CORPORATE SOURCE: Department of Chemistry, Lomonosov Moscow State University, Moscow 119899, Russia.
SOURCE: NUCLEIC ACIDS RESEARCH, (2001 Oct 1) 29 (19) 4062-9. Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20011001
Last Updated on STN: 20011029
Entered Medline: 20011025
AB Novel modified DNA duplexes with single bridging 5'-SS-monophosphoryldithio links [-OP(=O)-O(-)-SS-CH(2)-] were synthesized by **autoligation** of an oligonucleotide 3'-**phosphorothioate** and a 5'-mercapto-oligonucleotide previously converted to a 2-pyridyldisulfide adduct. Monophosphoryldisulfide link formation is not a stringent template-dependent process under the conditions used and does not require strong binding of the reactive oligomers to the complementary strand. The modified internucleotide linkage, resembling the natural phosphodiester bond in size and charge density, is stable in water, easily undergoes thiol-disulfide exchange and can be specifically cleaved by the action of reducing reagents. DNA molecules containing an internal

-OP(=O)-O(-)-SS-CH(2)- bridge are stable to spontaneous exchange of disulfide-linked fragments (recombination) even in the single-stranded state and are promising reagents for autocrosslinking with cysteine-containing proteins. The chemical and supramolecular properties of oligonucleotides with 5'-sulfhydryl groups were further characterized. We have shown that under the conditions of chemical ligation the 5'-SH group of the oligonucleotide has a higher reactivity towards N-hydroxybenzotriazole-activated phosphate in an adjacent oligonucleotide than does the OH group. This **autoligation**, unlike disulfide bond formation, proceeds only in the presence of template oligonucleotide, necessary to provide the activated phosphate in close proximity to the SH-, OH- or phosphate function.

L181 ANSWER 9 OF 33 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2001179848 MEDLINE
DOCUMENT NUMBER: 21110313 PubMed ID: 11175729
TITLE: Nonenzymatic **autoligation** in direct three-color detection of RNA and DNA point mutations.
AUTHOR: Xu Y; Karalkar N B; Kool E T
CORPORATE SOURCE: Department of Chemistry, University of Rochester, Rochester, NY 14627, USA.
CONTRACT NUMBER: GM60612 (NIGMS)
SOURCE: NATURE BIOTECHNOLOGY, (2001 Feb) 19 (2) 148-52. Journal code: 9604648. ISSN: 1087-0156.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010329

AB Enzymatic ligation methods are useful in diagnostic detection of DNA sequences. Here we describe the investigation of nonenzymatic **phosphorothioate**-iodide DNA **autoligation** chemistry as a method for detection and identification of both RNA and DNA sequences. Combining ligation specificity with the hybridization specificity of the ligated product is shown to yield discrimination of a point mutation as high as >10(4)-fold. Unlike enzymatic ligations, this reaction is found to be equally efficient on RNA or DNA templates. The reaction is also shown to exhibit a significant level of self-amplification, with the template acting in catalytic fashion to ligate multiple pairs of probes. A strategy for fluorescence labeling of three **autoligating** energy transfer (ALET) probes and directly competing them for **autoligation** on a target sequence is described. The method is tested in several formats, including solution phase, gel, and blot assays. The ALET probe design offers direct RNA detection, combining high sequence specificity with an easily detectable color change by fluorescence resonance energy transfer (FRET).

L181 ANSWER 10 OF 33 MEDLINE
ACCESSION NUMBER: 2001183735 MEDLINE
DOCUMENT NUMBER: 21170995 PubMed ID: 11277395
TITLE: Physical state of HPV16 and chromosomal mapping of the integrated form in cervical carcinomas.
AUTHOR: Kalantari M; Blennow E; Hagmar B; Johansson B
CORPORATE SOURCE: Division of Clinical Virology, Karolinska Institutet, Huddinge University Hospital, Sweden.. miki@labd01.hs.sll.se
SOURCE: DIAGNOSTIC MOLECULAR PATHOLOGY, (2001 Mar) 10 (1) 46-54.

Journal code: 9204924. ISSN: 1052-9551.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010510

AB Using a procedure based on restriction enzyme cleavage, **self-ligation**, and inverse polymerase chain reaction (rliPCR), the authors investigated 18 cervical intraepithelial neoplasia III (CIN III) cases and 37 invasive squamous carcinomas for integration of human papillomavirus type 16 (HPV16). All eighteen CIN III cases (severe dysplasia or high-grade squamous intraepithelial lesion) were found to harbor episomal HPV, but one of the samples contained mixed episomal and integrated forms. Seventeen of 37 invasive cervical carcinoma samples were identified previously as containing the completely integrated HPV16 genome by using PCR covering the entire E1/E2 gene, and this was confirmed by rliPCR in 16 cases. One case, however, showed a low level of episomal deoxyribonucleic acid in addition to the predominant integrated form. Of the remaining 20 carcinoma samples showing episomal forms in the previous analysis, 14 were found to contain integrated forms using rliPCR, and four contained multimeric episomal forms. Thus, in total, 31 of 37 of the carcinomas (84%) showed the integrated HPV16 genome. The rliPCR product from five carcinoma cases was cloned into a plasmid vector and used as a template for "primer walking" deoxyribonucleic acid sequencing to deduce human sequences flanking the integrated HPV genome. Based on this information, bacterial artificial chromosome (BAC) and P1-derived artificial chromosome (PAC) clones were obtained and used as probes in fluorescent in situ hybridization experiments on human metaphase chromosomes. The results of the fluorescent in situ hybridization experiments showed evidence for HPV16 integration in chromosome regions 1q25, 3q28, 6p25, 11p13, and 18q22. Sixteen carcinoma samples, containing episomal HPV16, were sequenced in the long control region. Evidence for changes in E2 binding or silencer YY1 sequences was found in only two samples.

L181 ANSWER 11 OF 33 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2000-628275 [60] WPIDS
DOC. NO. CPI: C2000-188262
TITLE: Detection of nucleic acid sequence differences for detecting cancer-associated mutations, germline mutations such as point mutation and infectious diseases by using ligase detection reaction with addressable arrays.
DERWENT CLASS: B04 D16
INVENTOR(S): BARANY, F; BARANY, G; DAY, J; GERRY, N P; HAMMER, R P; WITOWSKI, N E
PATENT ASSIGNEE(S): (CORR) CORNELL RES FOUND INC; (LOUU) UNIV LOUISIANA STATE & AGRIC & MECH COLL; (MINU) UNIV MINNESOTA
COUNTRY COUNT: 22
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000056927	A2	20000928	(200060)*	EN	217
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: AU CA JP					
AU 2000037545	A	20001009	(200103)		
EP 1208223	A2	20020529	(200243)	EN	

R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000056927	A2	WO 2000-US7006	20000317
AU 2000037545	A	AU 2000-37545	20000317
EP 1208223	A2	EP 2000-916438	20000317
		WO 2000-US7006	20000317

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000037545	A	Based on	WO 200056927
EP 1208223	A2	Based on	WO 200056927

PRIORITY APPLN. INFO: US 1999-125357P 19990319

AB WO 200056927 A UPAB: 20001123

NOVELTY - Identifying one or more sequences differing by one or more single-base changes, insertions, deletions or translocations in a large number of target nucleotide sequences (TNTS) by using a ligation phase, capture phase and a detection phase, is new.

DETAILED DESCRIPTION - Identifying one or more sequences differing by one or more single-base changes, insertions, deletions or translocations in a large number of target nucleotide sequences (TNTS) by using a ligation phase, capture phase and a detection phase, is new. The method comprises using a ligation phase (LP), capture phase and a detection phase. LP uses a **ligation detection reaction** between one oligonucleotide probe (ONTP) having a target sequence-specific portion and an addressable array-specific portion and a second ONTP having a target sequence-specific portion and a detectable label. The ONTPs in a particular set are suitable for ligation together when hybridized adjacent to one another on a corresponding TNTS but have a mismatch which differs with such ligation when hybridized to any other nucleotide sequence present in the sample. The LP is provided with a ligase which is blended with the sample to form a mixture and the mixture is subjected to one or more ligase detection reaction cycles comprising a denaturation treatment, where any hybridized oligonucleotides are separated from the TNTS and a hybridization treatment. The ONTP sets hybridize at adjacent positions in a base-specific manner to their respective TNTSs, if present in the sample and ligate to one another to form a ligated product sequence containing the addressable array-specific portion, the target-specific portions connected together, and the detectable reporter label. The capture phase involves hybridizing the ligated ONTPs to a solid support with an array of immobilized capture oligonucleotides at least some of which are complementary to the addressable array-specific portion. The labels of ligated ONTPs hybridized to the solid support are detected during the detection phase, which indicates the presence of one or more TNTS in the sample.

INDEPENDENT CLAIMS are also included for the following:

(1) an array of oligonucleotides on a solid support comprising a solid support having a porous surface and an array of positions each suitable for attachment of an oligonucleotide, a linker or support suitable for coupling an oligonucleotide to the solid support and an array of oligonucleotides on the solid support with at least some of the array positions being occupied by oligonucleotides more than 16 bases long; and

(2) a kit comprising a ligase, ONTP sets, and a solid support with a porous surface and capture oligonucleotides immobilized at particular

sites, where the oligonucleotides have nucleotide sequences complementary to the addressable array-specific portions.

USE - The method is useful for identifying sequences differing by one or more single base changes, insertions, deletions or translocations in large number of target nucleotide sequences. The method is useful for detection of, for e.g. cancer mutations, inherited (germline) mutations and infectious diseases. It is also useful in environmental monitoring, forensics and food science and also to detect plasmids containing genes that can metabolize xenobiotics, to monitor specific target microorganisms in population dynamic studies, or either to detect, identify or monitor genetically modified microorganisms in the environment and in industrial plants.

ADVANTAGE - A large number of nucleotide sequence differences in a sample can be detected at one time and multiplex analysis of complex genetic systems can be carried out efficiently. The method provides quantitative detection of mutations in a high background of normal sequences, allows detection of closely-clustered mutations, permits detection using addressable arrays and is amenable to automation.
Dwg.0/44

L181 ANSWER 12 OF 33 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2000315012 MEDLINE
DOCUMENT NUMBER: 20315012 PubMed ID: 10857023
TITLE: [Chemical ligation and recombination of DNA fragments by formation (exchange) of disulfide bonds, located in the sugar-phosphate backbone].
Khimicheskoe ligirovanie i rekombinatsiia fragmentov DNK posredstvom obrazovaniia (obmena) disul'fidnykh sviazei, lokalizovannykh v sakharofosfatnom ostove.
AUTHOR: Dolinnaia N G; Metelev V G
CORPORATE SOURCE: Moscow State University, Chemical Faculty, Moscow, Russia.. dolinnaya@biorg.chem.msu.su
SOURCE: BIOORGANICHESKAIA KHIMIIA, (2000 Apr) 26 (4) 306-14.
Journal code: 7804941. ISSN: 0132-3423.
PUB. COUNTRY: RUSSIA: Russian Federation
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Russian
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000720
Last Updated on STN: 20000720
Entered Medline: 20000712

AB Effective methods of the directed introduction of diphosphoryl disulfide bridges into hairpin DNA duplexes in place of natural phosphodiester groups were developed using the H2O2-effected ligation of 3'- and 5'-thiophosphorylated oligonucleotides or the **autoligation** of a preactivated oligonucleotide derivative with a **phosphorothioate** -bearing oligomer. The postsynthetic recombination of the disulfide-linked oligonucleotide fragments was characterized. It was shown that, along with template-directed reactions, out-of-duplex formation and exchange of diphosphoryl disulfide bonds in the DNA sugar-phosphate backbone may occur. In modified hairpin DNA, a spontaneous exchange of disulfide-linked fragments virtually does not take place because of the intramolecular duplex formation.

L181 ANSWER 13 OF 33 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:318925 HCAPLUS
DOCUMENT NUMBER: 133:161511
TITLE: Chemical ligation and recombination of DNA fragments through formation (exchange) of disulfide bonds

located in the sugar-phosphate backbone
AUTHOR(S): Dolinnaya, N. G.; Metelev, V. G.
CORPORATE SOURCE: Chemical Faculty, Moscow State University, Moscow, 119899, Russia
SOURCE: Russian Journal of Bioorganic Chemistry (Translation of Bioorganicheskaya Khimiya) (2000), 26(4), 277-284
CODEN: RJBCET; ISSN: 1068-1620
PUBLISHER: MAIK Nauka/Interperiodica
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Effective methods of the directed introduction of diphosphoryl disulfide bridges into hairpin DNA duplexes in place of natural phosphodiester groups were developed using the H2O2-effected ligation of 3'- and 5'-thiophosphorylated oligonucleotides or by **autoligation** of a preactivated oligonucleotide deriv. with a **phosphorothioate** -bearing oligomer. The postsynthetic recombination of the disulfide-linked oligonucleotide fragments was characterized. It was shown that, along with template-directed reactions, out-of-duplex formation and exchange of diphosphoryl disulfide bonds in the DNA sugar-phosphate backbone may occur. In modified hairpin DNA, a spontaneous exchange of disulfide-linked fragments virtually does not take place because of the intramol. duplex formation.
REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L181 ANSWER 14 OF 33 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 5
ACCESSION NUMBER: 2000:265584 BIOSIS
DOCUMENT NUMBER: PREV200000265584
TITLE: Polyphosphorylation and **non-enzymatic** **template**-directed **ligation** of **oligonucleotides**.
AUTHOR(S): Gao, Kui (1); Orgel, Leslie E. (1)
CORPORATE SOURCE: (1) Salk Institute for Biological Studies, San Diego, CA, 92186-5800 USA
SOURCE: Origins of Life and Evolution of the Biosphere, (Feb., 2000) Vol. 30, No. 1, pp. 45-51. print..
ISSN: 0169-6149.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB **Oligonucleotide** 5'-polyphosphates are formed under potentially prebiotic conditions from **oligonucleotide** 5'-phosphates and sodium trimetaphosphate. **Oligonucleotides** activated as polyphosphates undergo **template**-directed ligation. We believe that these reactions could have produced longer **oligonucleotide** products from shorter substrates under prebiotic conditions.

L181 ANSWER 15 OF 33 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 6
ACCESSION NUMBER: 2000:88331 BIOSIS
DOCUMENT NUMBER: PREV200000088331
TITLE: Nucleic acid duplexes incorporating a dissociable covalent base pair.
AUTHOR(S): Gao, Kui; Orgel, Leslie E. (1)
CORPORATE SOURCE: (1) Salk Institute for Biological Studies, 10010 North Torrey Pines Road, La Jolla, CA, 92037 USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (Dec. 21, 1999) Vol. 96, No. 26, pp. 14837-14842.

ISSN: 0027-8424.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB We have used molecular modeling techniques to design a dissociable covalently bonded base pair that can replace a Watson-Crick base pair in a nucleic acid with minimal distortion of the structure of the double helix. We introduced this base pair into a potential precursor of a nucleic acid double helix by chemical synthesis and have demonstrated efficient **nonenzymatic template**-directed **ligation** of the free hydroxyl groups of the base pair with appropriate short **oligonucleotides**. The **nonenzymatic ligation** reactions, which are characteristic of base paired nucleic acid structures, are abolished when the covalent base pair is reduced and becomes non-coplanar. This suggests that the covalent base pair linking the two strands in the duplex is compatible with a minimally distorted nucleic acid double-helical structure.

L181 ANSWER 16 OF 33 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 1999108155 MEDLINE
DOCUMENT NUMBER: 99108155 PubMed ID: 9889286
TITLE: High sequence fidelity in a non-enzymatic DNA **autoligation** reaction.
AUTHOR: Xu Y; Kool E T
CORPORATE SOURCE: Department of Chemistry, University of Rochester, Rochester, NY 14627, USA.
CONTRACT NUMBER: GM46625 (NIGMS)
SOURCE: NUCLEIC ACIDS RESEARCH, (1999 Feb 1) 27 (3) 875-81. Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990326
Last Updated on STN: 19990326
Entered Medline: 19990318
AB The success of oligonucleotide ligation assays in probing specific sequences of DNA arises in large part from high enzymatic selectivity against base mismatches at the ligation junction. We describe here a study of the effect of mismatches on a new non-enzymatic, reagent-free method for ligation of oligonucleotides. In this approach, two oligonucleotides bound at adjacent sites on a complementary strand undergo **autoligation** by displacement of a 5'-end iodide with a 3'-**phosphorothioate** group. The data show that this ligation proceeds somewhat more slowly than ligation by T4 ligase, but with substantial discrimination against single base mismatches both at either side of the junction and a few nucleotides away within one of the oligonucleotide binding sites. Selectivities of >100-fold against a single mismatch are observed in the latter case. Experiments at varied concentrations and temperatures are carried out both with the **autoligation** of two adjacent linear oligonucleotides and with intramolecular **autoligation** to yield circular 'padlock' DNAs. Application of optimized conditions to discrim-ination of an H- ras codon 12 point mutation is demonstrated with a single-stranded short DNA target.

L181 ANSWER 17 OF 33 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 8
ACCESSION NUMBER: 1999:144904 BIOSIS
DOCUMENT NUMBER: PREV199900144904

TITLE: Hairpin-shaped DNA duplexes with disulfide bonds in sugar-phosphate backbone as potential DNA reagents for crosslinking with proteins.
AUTHOR(S): Dolinnaya, Nina (1); Metelev, Valeri; Oretskaya, Tatiana; Tabatadze, David; Shabarova, Zoe
CORPORATE SOURCE: (1) Dep. Chem., Lomonosov Moscow State Univ., Moscow 119899 Russia
SOURCE: FEBS Letters, (Feb. 12, 1999) Vol. 444, No. 2-3, pp. 285-290.
ISSN: 0014-5793.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Convenient approaches were described to incorporate -OP(=O)O-SS-O-(O=PO- bridges in hairpin-shaped DNA duplexes instead of regular phosphodiester linkages: (i) H2O2- or 2,2'-dipyridyidisulfide-mediated coupling of 3'- and 5'- thiophosphorylated **oligonucleotides** on complementary **template** and (ii) more selective **template**-guided **autoligation** of a preactivated **oligonucleotide** derivative with an oligomer carrying a terminal thiophosphoryl group. Dithiothreitol was found to cleave completely modified internucleotide linkage releasing starting **oligonucleotides**. The presence of complementary **template** as an intrinsic element of the molecule protects the hairpin DNA analog from spontaneous exchange of disulfide-linked oligomer fragments and makes it a good candidate for auto-crosslinking with cysteine-containing proteins.

L181 ANSWER 18 OF 33 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:465161 HCAPLUS
DOCUMENT NUMBER: 129:230945
TITLE: Template-directed photoligation of oligodeoxyribonucleotides via 4-thiothymidine
AUTHOR(S): Liu, Jianquan; Taylor, John-Stephen
CORPORATE SOURCE: Department of Chemistry, Washington University in St Louis, St Louis, MO, 63130, USA
SOURCE: Nucleic Acids Research (1998), 26(13), 3300-3304
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Non-enzymic**, template-directed **ligation** of oligonucleotides in aq. soln. has been of great interest because of its potential synthetic and biomedical utility and implications for the origin of life. Though there are many methods for template-directed chem. ligation of oligonucleotides, there are only three reported photochem. methods. In the first report, template -directed photoligation was effected by cyclobutane dimer formation between the 5'- and 3'-terminal thymidines of two oligonucleotides with >290 nm light, which also damages DNA itself. To make the photochem. of native DNA more selective, we have replaced the thymidine at the 5'-end of one oligonucleotide with 4-thiothymidine (s4T) and show that it photoreacts at 366 nm with a T at the 3'-end of another oligonucleotide in the presence of a complementary template. When a single mismatch is introduced opposite either the s4T or its adjoining T, the ligation efficiency drops by a factor of five or more. We also show that by linking the two ends of the oligonucleotides together, photoligation can be used to form circular DNA mols. and to 'photopadlock' circular DNA templates. Thus, s4T-mediated photoligation may have applications to phototriggered anti-sense-based or antigen-based genetic tools, diagnostic agents and drugs, esp. for those situations in which chem. or enzyme-mediated ligation is undesirable or impossible, for example inside a cell.

L181 ANSWER 19 OF 33 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 9
ACCESSION NUMBER: 1998:496008 BIOSIS
DOCUMENT NUMBER: PREV199800496008
TITLE: Concept of "binary **oligonucleotide** reagent.
AUTHOR(S): Oshevski, S. I. (1)
CORPORATE SOURCE: (1) Inst. Cytol. Genet., Russ. Acad. Sci., Novosibirsk 630090 Russia
SOURCE: Nucleosides & Nucleotides, (Sept.-Nov., 1998) Vol. 17, No. 9-11, pp. 1969-1975.
ISSN: 0732-8311.
DOCUMENT TYPE: Article
LANGUAGE: English
AB A new strategy for site-directed chemical modification of NA is described. NA-**target**-driven **autoligation** reaction between two **oligonucleotide** derivatives with N(2-chloroethyl)-N-(p-formylphenyl)-N-propyl-N-3-ydeneamino and 4-carbohydrazidephenyl groups at their opposing termini results in the NA-**target** modification, which is several times more effective than modification by one of the derivatives.

L181 ANSWER 20 OF 33 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: ~~1998:192838~~ HCAPLUS
DOCUMENT NUMBER: 128:283027
TITLE: Nucleosides and nucleotides. 165. Chemical ligation of oligodeoxyribonucleotides having a mercapto group at the 5-position of 2'-deoxyuridine via a disulfide bond
AUTHOR(S): Ueno, Yoshihito; Nakagawa, Aiko; Matsuda, Akira
CORPORATE SOURCE: Fac. Pharmaceutical Sci., Hokkaido Univ., Saporo, 060, Japan
SOURCE: Nucleosides & Nucleotides (1998), 17(1-3), 283-289
CODEN: NUNUD5; ISSN: 0732-8311
PUBLISHER: Marcel Dekker, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We describe the **nonenzymic ligation** of oligodeoxynucleotides (ODNs) contg. a mercapto group at the 5-position of 2'-deoxyuridine via a disulfide bond. Two ODNs contg. different sequences were efficiently ligated in the presence of a template by this method.

L181 ANSWER 21 OF 33 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 1997-435273 [40] WPIDS
DOC. NO. NON-CPI: N1997-362008
DOC. NO. CPI: C1997-139710
TITLE: Detecting single-base variations in target nucleic acid by ligase detection reaction with probe pair - then capture on array of immobilised oligonucleotides, used to diagnose infections, genetic disease and cancer, allows many targets to be detected in single array.
DERWENT CLASS: A89 B04 C07 D13 D16 J04 S03
INVENTOR(S): BARANY, F; BARANY, G; BLOK, H; HAMMER, R P; KEMPE, M; ZIRVI, M
PATENT ASSIGNEE(S): (CORR) CORNELL RES FOUND INC; (LOUU) UNIV LOUISIANA STATE; (MINU) UNIV MINNESOTA
COUNTRY COUNT: 75
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

WO 9731256 A2 19970828 (199740)* EN 124
RW: AT BE CH DE DK EA ES FI FR GB GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK TJ TM TR TT UA UG US UZ VN
AU 9727997 A 19970910 (199802)
WO 9731256 A3 19970925 (199814)
EP 920440 A2 19990609 (199927) EN
R: CH DE FR GB IT LI SE
AU 735440 B 20010705 (200143)
JP 2001519648 W 20011023 (200202) 154

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9731256	A2	WO 1997-US1535	19970205
AU 9727997	A	AU 1997-27997	19970205
WO 9731256	A3	WO 1997-US1535	19970205
EP 920440	A2	EP 1997-922283	19970205
		WO 1997-US1535	19970205
AU 735440	B	AU 1997-27997	19970205
JP 2001519648	W	JP 1997-530164	19970205
		WO 1997-US1535	19970205

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9727997	A	Based on	WO 9731256
EP 920440	A2	Based on	WO 9731256
AU 735440	B	Previous Publ.	AU 9727997
		Based on	WO 9731256
JP 2001519648	W	Based on	WO 9731256

PRIORITY APPLN. INFO: US 1996-11359P 19960209

AB WO 9731256 A UPAB: 19971006
A method for detecting at least one of a plurality of sequences (A) differing by one or more single-base changes, insertions, deletions or translocations in many target sequences comprises: (a) combining: (i) a sample potentially containing one or more target nucleotide sequences with a plurality of sequence differences; (ii) many sets of oligonucleotide probes (B), each set having one probe (P1) with a target-specific part (TSP) and an addressable array-specific part (AASP) and second probe (P2) with a TSP and a detectable reporter label (RL), P1 and P2 of each set being ligatable when hybridised adjacent to one another on the target sequence but having a mismatch that prevents ligation on any other sequence in the sample; and (iii) ligase; (b) subjecting the mixture to at least one **ligation detection reaction** (LDR) cycle comprising denaturation and hybridisation/ligation so that if the appropriate target sequence is present a ligation product will be formed containing the AASP, both TSP (ligated together) and RL; the probes may hybridise to other sequences but ligation will not then occur; (c) applying the reaction mixture to a solid support having different capture oligonucleotides (CON), complementary to AASP, immobilised at specific sites; and (d) detecting RL of ligation products captured by the array. Also new are: (1) method for forming arrays of CON on a solid support; (2) CON arrays produced using the method of (1); and (3) kits for use in the above methods.

USE - The method is used to diagnose bacterial, viral, parasitic or fungal infection (e.g. E. coli, Candida albicans, human immunodeficiency virus, Plasmodium falciparum and many others). The method can also be used for the diagnosis of genetic diseases (e.g. cystic fibrosis, fragile X syndrome etc.) or cancers associated with oncogenes, tumour suppressors or other genes involved in DNA amplification, repair, replication and recombination. The method is particularly useful in environmental monitoring, forensic science and monitoring of foods and feeds.

ADVANTAGE - Presence, or absence, of many selected sequences can be detected rapidly on a single array, and the method can be made quantitative. By combining the sensitivity of polymerase chain reaction (PCR) with the specificity of LDR, problems of allele-specific PCR, such as false positives, primer interference, poor suitability for automation, are overcome. The capture array can be regenerated for reuse.
Dwg.3/34

L181 ANSWER 22 OF 33 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1997:553496 HCAPLUS
DOCUMENT NUMBER: 127:248352
TITLE: A novel 5'-iodonucleoside allows efficient **nonenzymic ligation** of single-stranded and duplex DNAs
AUTHOR(S): Xu, Yanzheng; Kool, Eric T.
CORPORATE SOURCE: Dep. Chem., Univ. Rochester, Rochester, NY, 14627, USA
SOURCE: Tetrahedron Letters (1997), 38(32), 5595-5598
CODEN: TELEAY; ISSN: 0040-4039
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A new iodothymidine phosphoramidite enables the placement of a 5'-iodide into oligodeoxyribonucleotides; the iodide is stable to ammonia deprotection and allows **nonenzymic ligations** of DNA.

L181 ANSWER 23 OF 33 MEDLINE
ACCESSION NUMBER: 97323009 MEDLINE
DOCUMENT NUMBER: 97323009 PubMed ID: 9179499
TITLE: Cloning of the promoter regions of mouse TGF-beta receptor genes by inverse PCR with highly overlapped primers.
AUTHOR: Yoshitomo-Nakagawa K; Muramatsu M; Sugano S
CORPORATE SOURCE: Department of Virology, University of Tokyo, Japan.
SOURCE: DNA RESEARCH, (1997 Feb 28) 4 (1) 73-5.
Journal code: 9423827. ISSN: 1340-2838.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199708
ENTRY DATE: Entered STN: 19970813
Last Updated on STN: 19970813
Entered Medline: 19970806
AB In order to isolate promoters of mouse TGF-beta receptor genes, we used inverse PCR with highly overlapped primers corresponding to the 5' sequence of the receptor cDNAs. Nested primer sets only covered a 30- to 40-base region of the sequences. HinfI-digested and **self-ligated** mouse genomic DNA was used as a PCR template. Only one band for each receptor was seen after PCR. The amplified DNA fragments could direct luciferase production when the luciferase coding sequence was ligated after the fragments. The sequence of the fragment which correspond to the type II receptor showed partial homology with the promoter region of the human TGF-beta type II receptor. Thus, the inverse PCR with highly

overlapped primers could be an easy way to isolate the promoter regions of many genes.

L181 ANSWER 24 OF 33 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 1996-259864 [26] WPIDS
DOC. NO. CPI: C1996-082356
TITLE: Multiplex **ligation dependent amplification** - used to detect target nucleic acid sequence and specifically amplify multiple target sequences using single primer pair..
DERWENT CLASS: B04 D16
INVENTOR(S): CARRINO, J J
PATENT ASSIGNEE(S): (ABBO) ABBOTT LAB
COUNTRY COUNT: 18
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9615271	A1	19960523	(199626)*	EN	38

RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
W: CA JP

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9615271	A1	WO 1995-US14886	19951115

PRIORITY APPLN. INFO: US 1994-344203 19941116
AB WO 9615271 A UPAB: 19960705
Amplifying a target nucleic acid sequence (I) is new, which comprises: (a) forming a reaction mixture under hybridising conditions with: (i) a sample suspected of contg. a target strand (TS) with a target sequence of interest, the TS being present in single stranded form; (ii) at least 1 split probe (SP) having a 5' end complementary to a first segment of the TS and a 3' end complementary to a second segment of the TS, the second segment being sufficiently near the first segment such that the 5' end can be joined to the 3' end when the SP reagent is hybridised with the TS, where the 5' and the 3' end are on two distinct polynucleotides (PN) or on different ends of one continuous PN; the SP reagent further having a first non-complementary region located downstream of the 5' end and not complementary to the TS, and a second non-complementary region located upstream of the 3' end and not complementary to the TS; and (iii) an agent for ligating together the 3' and 5' ends of the SP reagent; (b) ligating together the 3' and 5' ends of the SP reagent while hybridised with the TS to form a ligated probe having a ligation junction; (c) sepg. the ligated probe from the TS; (d) treating the reaction mixt. under hybridising conditions with: (i) an excess of amplification primers (P) where the first P has a sequence complementary to a primer binding site (PBS) located in the non-complementary region; and where a second P has a sequence identical to a PBS located in the second non-complementary region, with the proviso that if the SP reagent is continuous the PBS located in the first non-complementary region is upstream of the PBS located in the second non-complementary region; (ii) a supply of deoxynucleotide triphosphates; and (iii) an agent for inducing extension of the Ps; (e) an agent for inducing extension of the Ps to form an extension product from it; (f) treating the reaction mixt. under denaturing conditions to separate P extension products from their templates; (g) treating the reaction mixt. under hybridising conditions to

anneal the Ps to the ligated probe or to extension prod. of the first P and extending the Ps to form extension products from it.
USE - The methods are used to amplify and detect a target nucleic acid sequence and to specifically amplify multiple target sequences using a single pair of primers.
Dwg.0/4

L181 ANSWER 25 OF 33 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1996:390826 BIOSIS
DOCUMENT NUMBER: PREV199699113182
TITLE: Circular **oligonucleotides**: New concepts in **oligonucleotide** design.
AUTHOR(S): Kool, Eric T.
CORPORATE SOURCE: Dep. Chem., Univ. Rochester, Rochester, NY 14627 USA
SOURCE: Stroud, R. M. [Editor]. Annual Review of Biophysics and Biomolecular Structure, (1996) Vol. 25, pp. 1-28. Annual Review of Biophysics and Biomolecular Structure. Publisher: Annual Reviews Inc. P.O. Box 10139, 4139 El Camino Way, Palo Alto, California 94306, USA. ISSN: 1056-8700. ISBN: 0-8243-1825-0.
DOCUMENT TYPE: Book; General Review
LANGUAGE: English

L181 ANSWER 26 OF 33 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.
ACCESSION NUMBER: 1996:26197492 BIOTECHNO
TITLE: Circular oligonucleotides: New concepts in oligonucleotide design
AUTHOR: Kool E.T.
CORPORATE SOURCE: Department of Chemistry, University of Rochester,Rochester, NY 14627, United States.
SOURCE: Annual Review of Biophysics and Biomolecular Structure, (1996), 25/- (1-28) CODEN: ABBSE4 ISSN: 1056-8700
DOCUMENT TYPE: Journal; General Review
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Recent progress in the synthesis and properties of circular oligonucleotides as ligands for DNA and RNA and as templates for polymerase enzymes is described. Small synthetic circular DNAs, RNAs, and chimeric analogues ranging from 28 to 74 nucleotides in size have been synthesized with the use of a **nonenzymatic ligation** strategy. Some of these were designed to undergo triplex formation with single-stranded DNA and RNA targets, and many bind with affinities and sequence selectivities considerably greater than those seen for linear oligonucleotides. Design strategies and modes of binding are discussed in the light of possible use of such molecules as **hybridization** probes, molecular diagnostics, and sequence-specific inhibitors of gene expression. Small circular oligonucleotides have also been shown to act as unusually efficient templates for DNA and RNA polymerases, which produce long, repeating copies of the circular sequence by a rolling circle process.

L181 ANSWER 27 OF 33 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1995:808924 HCAPLUS
DOCUMENT NUMBER: 124:146687
TITLE: A Covalent Lock for Self-Assembled Oligonucleotide Conjugates
AUTHOR(S): Herrlein, Mathias K.; Nelson, Jeffrey S.; Letsinger, Robert L.

CORPORATE SOURCE: Department of Chemistry, Northwestern University, Evanston, IL, 60208, USA
SOURCE: J. Am. Chem. Soc. (1995), 117(40), 10151-2
CODEN: JACSAT; ISSN: 0002-7863
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Oligonucleotide conjugates have potential as components in creating self-assembling supramol. systems. Since the hybridization reactions are reversible, convenient procedures for locking such systems in place after assembly can be useful. We describe here a hybridization dependent **autoligation** that affords a bridge [-OP(O)(O-)S-] very close in geometry and charge distribution to a natural phosphodiester link. The coupling, utilizing displacement of a 5'-O-tosyl group by a 3'-**phosphorothioate**, is shown to be remarkably selective and efficient when the structural units are appropriately organized. This approach is illustrated with three different systems: conversion of a linear oligomer to a dumbbell oligodeoxyribonucleotide, intramol cyclocondensation of an oligodeoxyribonucleotide-stilbene dicarboxamide conjugate possessing mismatches and a very short overlap at the juncture site, and closure of a stilbene dicarboxamide cap at the end of a duplex. These examples show that although the coupling depends strongly on proper organization of the component blocks, the latitude in the geometrical constraints is sufficient to permit efficient coupling in oligonucleotide systems differing substantially from those conventionally employed in ligation.

L181 ANSWER 28 OF 33 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 10
ACCESSION NUMBER: 1995:340343 BIOSIS
DOCUMENT NUMBER: PREV199598354643
TITLE: **Autoligation** of **oligonucleotides** via nucleophilic substitution reaction.
AUTHOR(S): Gryaznov, Sergei M.
CORPORATE SOURCE: Lynx Ther. Inc., 3832 Bay Center Place, Hayward, CA 94545 USA
SOURCE: Nucleosides & Nucleotides, (1995) Vol. 14, No. 3-5, pp. 1019-1022.
ISSN: 0732-8311.
DOCUMENT TYPE: Article
LANGUAGE: English

AB A fast and efficient **template** - driven **autoligation** reaction between **oligonucleotides** derivatized with bromoacetyl and thiol groups at their opposing termini is described. The product of reaction is capable of forming a stable duplex with a complementary DNA strand.

L181 ANSWER 29 OF 33 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 11
ACCESSION NUMBER: 1995:77817 BIOSIS
DOCUMENT NUMBER: PREV199598092117
TITLE: Selective chemical **autoligation** on a double-stranded DNA **template**.
AUTHOR(S): Herrlein, Mathias K.; Letsinger, Robert L. (1)
CORPORATE SOURCE: (1) Dep. Chem., Northwestern Univ., Evanston, IL 60208 USA
SOURCE: Nucleic Acids Research, (1994) Vol. 22, No. 23, pp. 5076-5078.
ISSN: 0305-1048.
DOCUMENT TYPE: Article
LANGUAGE: English

AB We show that a double-stranded DNA segment serves as an effective

template for spontaneously coupling short pyrimidine **oligonucleotides** containing terminal -P(O)(O-)S- and BrCH-2C(O)NH- groups. The efficiency of this **autoligation** depends markedly on proper base-pairing between the **probe** oligomers and the double-stranded **target**. This chemistry should be useful in designing highly selective **probes** for double-stranded **polynucleotide** segments.

L181 ANSWER 30 OF 33 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 94310066 MEDLINE
DOCUMENT NUMBER: 94310066 PubMed ID: 8036165
TITLE: Enhancement of selectivity in recognition of nucleic acids via chemical **autoligation**.
AUTHOR: Gryaznov S M; Schultz R; Chaturvedi S K; Letsinger R L
CORPORATE SOURCE: Lynx Therapeutics Inc., Hayward, CA 94545.
CONTRACT NUMBER: 10265 (NIAID)
UOI AI24846
SOURCE: NUCLEIC ACIDS RESEARCH, (1994 Jun 25) 22 (12) 2366-9.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199408
ENTRY DATE: Entered STN: 19940825
Last Updated on STN: 19940825
Entered Medline: 19940815

AB A new approach to increase the selectivity of interaction between oligonucleotide probes and target nucleic acids is described. In place of a single, relatively long oligonucleotide probe, two or three short oligomers terminated by thiophosphoryl and bromoacetamido groups are employed. Fast and efficient **autoligation** takes place when the oligomers hybridize in a contiguous mode to the same complementary strand such that a thiophosphoryl group on one strand and a bromoacetamido group on another are brought into proximity. A single nucleotide mismatch for the short probes leads to marked reduction in the rate of **autoligation**. The binding affinity of the product is close to that for a natural probe of the same length. This approach could have potential in oligonucleotide-based diagnostics, chemical amplification systems, and therapeutic applications.

L181 ANSWER 31 OF 33 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1992:505279 HCAPLUS
DOCUMENT NUMBER: 117:105279
TITLE: **Nonenzymic ligation** of double-helical DNA by alternate-strand triple helix formation
AUTHOR(S): Luebke, Kevin J.; Dervan, Peter B.
CORPORATE SOURCE: Arnold and Mabel Beckman Lab. Chem. Synth., California Inst. Technol., Pasadena, CA, 91125, USA
SOURCE: Nucleic Acids Res. (1992), 20(12), 3005-9
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English

AB **Nonenzymic ligation** of double-stranded DNA has been performed using an alternate-strand binding oligodeoxyribonucleotide template to juxtapose the duplex termini in a triple helical complex. The template assocs. with the duplex termini by Hoogsteen hydrogen bonding to alternate strands on opposite sides of the ligation site. Intermol. and intramol. ligation of linearized plasmid DNA are obsd. in the reaction,

which depends on the template oligodeoxyribonucleotide and a condensing agent, N-cyanoimidazole. Intramol. ligation products include those in which both strands are covalently closed in a circle. Ligation of the two strands is sequential and occurs at comparable rates for the first and second strands ligating. The covalent linkages formed in the reaction can be cleaved by the restriction endonuclease StuI, supporting their identification as phosphodiesters.

L181 ANSWER 32 OF 33 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1991:530958 HCAPLUS
DOCUMENT NUMBER: 115:130958
TITLE: **Nonenzymic** sequence-specific **ligation** of double-helical DNA
AUTHOR(S): Luebke, Kevin J.; Dervan, Peter B.
CORPORATE SOURCE: Arnold and Mabel Beckman Lab. Chem. Synth., California Inst. Technol., Pasadena, CA, 91125, USA
SOURCE: J. Am. Chem. Soc. (1991), 113(19), 7447-8
CODEN: JACSAT; ISSN: 0002-7863
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The 5'-phosphate and 3'-hydroxyl termini of 2 DNA duplexes are aligned for condensation by assocn. of a 3rd strand template in a triple helical complex. Ligation of the duplexes occurs following activation of the terminal 5'-phosphates in this complex by using N-cyanoimidazole as condensing agent. A linear plasmid DNA (3.7 kilobase pairs) can be circularized covalently in >60% yield. The yield of plasmid ligated on both strands is >15%. The reaction requires the oligodeoxyribonucleotide template. The sequence specificity of the template strand for each duplex end confers sequence specificity to the ligation reaction.

L181 ANSWER 33 OF 33 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1989:628491 HCAPLUS
DOCUMENT NUMBER: 111:228491
TITLE: **Nonenzymatic ligation** of oligodeoxyribonucleotides on a duplex DNA template by triple-helix formation
AUTHOR(S): Luebke, Kevin J.; Dervan, Peter B.
CORPORATE SOURCE: Arnold and Mabel Beckman Lab. Chem. Synthesis, California Inst. Technol., Pasadena, CA, 91125, USA
SOURCE: J. Am. Chem. Soc. (1989), 111(23), 8733-5
CODEN: JACSAT; ISSN: 0002-7863
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A double-stranded DNA template can direct the sequence-specific formation of a phosphodiester linkage between pyrimidine oligodeoxynucleotides in aq. soln. by juxtaposing the oligonucleotide termini head-to-tail in a triple helical complex. Within the context of the development of chem. systems for macromol. information transfer, triple helix-directed ligation can create sequences that are neither identical nor complementary in a Watson-Crick sense to the template, but rather new sequences of nucleic acids.